

## **FIGURE 1**

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGCTGGTAAGGATTACAAAAGGTGCAGGTATG  
AGCAGGTCTGAAGACTAACATTGTGAAGTTGTAACAGAAAACCTGTTAGAAATGGGTGGT  
TTCAGCAAGGCCTCAGTTCTTCTCAGCCCTGTAATTGGACATCTGCTGCTTCATATTT  
TCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTACCTTATATCAGTGACACTGG  
TACAGTAGCTCCAGAAAAATGCTTATTGGGCAATGCTAAATATTGCGGCAGTTTATGCATTG  
CTACCATTATGTCGTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAGAACGTTATCATCAA  
TTAAACAAGGCTGGCCTTGACTTGAATACTGAGTTAGGACTTCTATTGTGGCAAACCTT  
CCAGAAAACAACCCTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTGGTATGGCTCAT  
TATATATGTTGTCAGACCACCTTCTACCAAATGCAGCCAAAATCCATGGCAAACAAAGTC  
TTCTGGATCAGACTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTC  
ATCAGTTTGACAGTGGCAATTGGACTGATTAGAACAGAAAACCTCCATTGAAACCCGAGG  
ACAAAGTTATGTGCTTCACATGATCACTACTGCAGCAGAATGGTCTATGTCATTCTTCTT  
GGTTTCTGACTTACATTGATTTCAAGAAAATTCTTACGGGTGAAAGCCAATTACA  
TGGATTAACCCTATGACACTGCACCTGCCCTATTAAACATGAACGAACACGGCTACTTCCA  
GAGATATTGATGAAAGGATAAAATATTCTGTAATGATTGATTCTCAGGGATTGGGAAAGG  
TTCACAGAAGTTGCTTATTCTCTGAAATTCAACCACTTAATCAAGGCTGACAGTAACACT  
GATGAATGCTGATAATCAGGAAACATGAAAGCCATTGATAGATTATTCTAAAGGATATCAT  
CAAGAAGACTATTAAAACACCTATGCCTATACCTTTTATCTCAGAAAATAAGTCAAAGACT  
ATG

## **FIGURE 2**

<subunit 1 of 1, 266 aa, 1 stop

<MW: 29766, pI: 8.39, NX(S/T): 0

MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAV  
LCIATIYVRYKQVHALSPEENVIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTG  
MGSLYMFVQTILSYQMOPKIHGKQVFIRLLLVIWCGVSALSMTCSSVLHSGNFGTDLEQKLHW  
NPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFQKISLRVEANLHGLTLYDTAPCPINNERTR  
LLSRDI

**Important features:**

**Type II transmembrane domain:**

amino acids 13-33

**Other Transmembrane domains:**

amino acids 54-73, 94-113, 160-180, 122-141

**N-myristoylation sites.**

amino acids 57-63, 95-101, 99-105, 124-130, 183-189

### **FIGURE 3**

CGGACGCGTGGCGGACGCGTGGGGAGAGCCGAGTCCCGCTGCAGCACCTGGAGAAGGCAGACC  
GTGTGAGGGGGCCTGTGGCCCCAGCGTGTGGCTCGGGAGTGGAAAGTGGAGGCAGGAGCCTTC  
CTTACACTTCGCCATGAGTTTCCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTG  
GATTTGGGTGGCTTCTCATGCGCAATTGTTAAAGACTATGAGATACTGAGTCAGTATGTTGTACAG  
GTGATCTCTCCGTGACGTTGCATTTCTGCACCATGTTGAGCTCATCATCTTGAAATCTTAGG  
AGTATTGAATAGCAGCTCCCGTTATTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGG  
TTTCATGGTGCCTTTACATTGGCTATTTATTGTGAGCAATATCCACTACTGCATAAACACGA  
CTGCTTTTCTGTCTTATGGCTGACCTTATGTATTCTCTGGAAACTAGGAGATCCCTTCC  
CATTCTCAGCCAAAACATGGATCTTATCCATAGAACAGCTCATGCCGTTGGTGTGATTGGAG  
TGAECTCATGGCTCTTCTGGATTGGTGTCACTGCCATACACTTACATGTCTTACTTC  
CTCAGGAATGTGACTGACACGGATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGAT  
CATAAAGCAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGAAGTGCATAACA  
AACCATCAGGTTCTGGGAATGATAAAAGTGTACCACTCAGCATCAGGAAGTGAAGGAAATCTTACT  
CTTATTCAACAGGAAGTGGATGCTTGGAAAGAATTAAGCAGGCAGCTTCTGGAAACAGCTGATCT  
ATATGCTACCAAGGAGAGAATAGAAACTCCAAACCTTCAAGGGAAATATTTAATTTCCTGGTT  
ACTTTTCTCTATTACTGTGTTGGAAAATTTCATGGCTACCATCAATATTGTTTGATCGAGTT  
GGGAAAACGGATCTGTACAAGAGGCATTGAGATCACTGTGAATTATCTGGAAATCCAATTGATGT  
GAAGTTTGGTCCAACACATTCTCATTCTGGATAATCATCGTCACATCCATCAGAGGAT  
TGCTGATCACTCTAACCAAGTCTTTATGCCATCTAGCAGTAAGTCTCCAATGTCATTGCTCTG  
CTATTAGCACAGATAATGGCATGTACTTGTCTCCTGTGCTGATCCGAATGAGTATGCCTT  
AGAATACCGCACCATTAATCACTGAAGTCTGGAGAACTGCAGTTCAACTCTATCACCGTTGGTTG  
ATGTGATCTCCTGGTCAGCGCTCTCTAGCATACTCTTCTCTATTGGCTCACAAACAGGCACCA  
GAGAAGCAAATGGCACTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTCAAAATTAA  
GATATAAGAGGGGGAAAATGGAACCAGGGCTGACATTAAACAAACAAATGCTATGGTAGC  
ATTTTCACCTTCATAGCATACTCCTCCCGTCAGGTGATACTATGACCATGAGTACGATCAGCCAG  
AACATGAGAGGGAGAGAACTAACTCAAGACAATACTCAGCAGAGAGCATCCGTGTGGATATGAGGCTGG  
TGTAGAGGCGGAGAGGAGCCAAGAAACTAAAGGTGAAAATACACTGGAACCTGTTAGCTGGCAAGACATGT  
CTATGGTAGCTGAGCCAACACGTTAGGATTCGTTTAAGGTTCACATGGAAAGGTTAGCTTGC  
CCTTGAGATTGACTCATTAAACAGAGACTGTAACAAAAAAAAGGGCGGCCGCG  
ACTCTAGAGTCGACCTGCAGAAGCTGGCCGCAACTGTTATTGCAGCTATAATG

## **FIGURE 4**

MSFLIDSSIMITSQILFFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGV  
LNSSSRYFHWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGDP  
FPILSPKKGILSIEQLISRVGVIGVTLMAILSGFGAVNCPTYMSYFLRNVTDDILALERRLQ  
TMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQQEVDALEELSRQ  
LFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVFDRVGKTDPVTRGIEI  
TVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLKFFYAISSSKSSNVIVLLAQMIMGMY  
FVSSVLLIRMSMPLYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPEKQMAP

**Important features:**

**Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

## **FIGURE 5**

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGTTCC  
AGAACTCTCATCCGACTAGTTATTGAGCATCTGCCTCTATATCACCAAGTGGCCATCTGAGGT  
GTTTCCCTGGCTCGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGGCTTCTCACT  
TCCATCTGGACCAAGGGCTCTGGTCAAGGCTTTGCGTGCAGAAGAGCTTCCATCCAGGT  
GTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCGAGCTGAATTTCACAG  
AAGCTAAGGAGGCCGTAGGCTGCTGGGACTAAGTTGCCGGCAAGGACCAAGTTGAAACAGCC  
TTGAAAGCTAGCTTGAAACTTGCACTATGGCTGGGAGATGGATTGTTGCTGATCTCTAG  
GATTAGCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTCTGATTGGAAGGTTCCAGTGA  
GCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGATACTTGGACTAACTCGTGCATTCCAGAA  
ATTATCACCAACAAAGATCCCATATTCAACACTCAAACCTGCAACACAAACAGAATTATG  
CAGTGACAGTACCTACTCGGTGGCATCCCTTACTCTACAATACCTGCCCTACTACTCCTC  
CTGCTCCAGCTTCCACTTCTATTCCACGGAGAAAAAAATTGATTGTCACAGAAGTTTATG  
GAAACTAGCACCATGTCTACAGAAACTGAACCAATTGTTGAAAATAAGCAGCATTCAGAATGA  
AGCTGCTGGGTTGGAGGTGTCCCCACGGCTCTGCTAGTGCTGCTCTCTCTTGGTGTG  
CAGCTGGCTTGATTTGCTATGTCAAAAGGTATGTAAGGGCTTCCCTTTACAAACAAGAAT  
CAGCAGAAGGAAATGATCGAAACCAAAGTAGTAAGGAGGAGAACGGCAATGATAGCAACCTAA  
TGAGGAATCAAAGAAAATGATAAAAACCCAGAAGACTCCAAGAGTCCAAGCAAAACTACCGTGC  
GATGCCCTGGAAGCTGAAGTTAGATGAGACAGAATGAGGAGACACACCTGAGGCTGGTTCTT  
CATGCTCCTTACCCCTGCCCAAGCTGGGAAATCAAAGGGCAAAGAACCAAAGAAGAAAGTCCA  
CCCTGGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAT  
GCCCTTCTCCTTATGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCT  
TTCTAGGCTGGCTATGCTTAATAATATCCACTGGGAGAAAGGAGTTGCAAAGTGCAGGAC  
CTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCTCTGGCTGCTGAGGCTAGGTGGTTG  
AAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGACCCCTTCTCA  
GCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCCTCTGAGGCCGTAAGAGCAAAAGAAT  
GGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAGACCTAATCTGTAAA  
GCTAAAATAAGAAATAGAACAGGCTGAGGATACGACAGTACACTGTCAGCAGGACTGTAAAC  
ACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGAATCTGTTAGAACACACACA  
CTTACTTTCTGGTCTCTACCACTGCTGATATTTCTAGGAAATACTTTACAAGTAACA  
AAAATAAAAATCTTATAAAATTCTATTCTGAGTTACAAGAATGATTACTAAGGAAGATT  
ACTCAGTAATTGTTAAAAGTAATAAAACATTTGCTGAATAGCTACTATATGTC  
AAAGTGTGTGCAAGGTATTACACTCTGTAATTGAATATTCTGCTAAAGGCTTCTGAACT  
AACGCTATCTGGGAAGCTATTCTGAGTTGATATTCTAGCTTATCTACTTCCAAACTAAT  
TTTATTTGCTGAGACTAATCTTATTCTCATTTCTAATATGCCAACATTATAACCTTAATT  
TATTATAACACCTAACAGAAGTACATTGTTACCTATACCAAGCACATTAAAAGTGCC  
ATTAACAAATGTATCACTAGCCCTCTTTCAACAGAACAGGACTGAGAGATGCAGAAATATT  
TGTGACAAAAATTAAAGCATTTAGAAAACCTT

## **FIGURE 6**

MARCFSLVLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLLG  
LSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNCGKNGVGVLIWKPVSRQFAAYCYN  
SSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTPPAPASTSIPR  
RKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFFGAAAGLGFYVK  
RYVKAFFPTNKNQQKEMIETKVVKEEKANDSNPNEESKTDKNPEESKSPSKTTVRCLEAEV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 235-254

**N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

**Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

**Tyrosine kinase phosphorylation site.**

amino acids 79-88

**N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## **FIGURE 7**

CGCCGCGCTCCCGCACCGCGGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCCCGGC  
GCCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGAGCGCAACTCGGTCCAGTCGGGGCG  
CGGCTGCGGGCGCAGAGCGGAGATGCAGCGCTTGGGGCCACCCCTGCTGTGCTGCTGCTGGCG  
CGGCGGTCCCCACGGCCCCCGGCCCGCTCCGACGGCACCTCGGCTCCAGTCAGCAGCCCCGG  
GCTCTCAGCTACCCGAGGAGGCCACCTCAATGAGATGTTCCGAGGGTTGAGGAAGTGT  
GGAGGAACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGGCAGAAGAAGCTGCTGTA  
AAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTATCACAATGAGACCAACACAGAC  
ACGAAGGTTGGAATAATACCATCCATGTGACCGAGAAATTCAAGATAACCAACAACCAGAC  
TGGACAATGGTCTTTCAGAGACAGTTACATCTGTGGGAGACAGAAGAAGGCAGAAGGAGCC  
ACGAGTGCATCATCGACGAGGAAGTGTGGGCCAGCATGTAAGTGCAGTTGCCAGCTCCAGTAC  
ACCTGCCCCAGCCATGCCGGGGCCAGAGGATGCTCTGCACCCGGGACAGTGAAGTGTGGAGACCA  
GCTGTGTCTGGGGTCACTGCACCAAAATGGCCACCAGGGGAGCAATGGGACCATCTGTGACA  
ACCAGAGGGACTGCCAGCCGGGGCTGTGCTGTGCTTCAGAGAGGGCTGCTGTCCCTGTG  
ACACCCCTGCCGTGGAGGGCGAGCTTGCATGACCCGCCAGCCGGCTCTGGACCTCATCAC  
CTGGGAGCTAGAGCTGTGGAGCCTGGACCGATGCCCTGTGCTGCAGTGGCCTCCTCTGCCAGC  
CCCACAGCCACAGCCTGGTGTATGTGCAAGCCGACCTTGTGGGAGCCGTGACCAAGATGGG  
GAGATCCTGCTGCCAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTG  
CCAGGAGCTGGAGGAACCTGGAGAGGAGCCTGACTGAAGAGATGGCCTGGGGAGCCTGCG  
CCGCCGCTGCACTGCTGGAGGGGAAGAGATTAGATCTGGACAGGCTGTGGTAGATGTGCAA  
TAGAAATAGCTAATTATTCAGGTGTTGCTTAGGCGTGGGCTGACAGGCTTCTCT  
CATCTCTCCAGTAAGTTCCCTCTGGCTGACAGCATGAGGTGTTGCTGATTGTCAGT  
CCCCCAGGCTGTTCTCCAGGCTCACAGTCTGGTGTGCTGGGAGAGTCAGGCAGGGTTAAACTGCA  
GGAGCAGTTGCCACCCCTGTCCAGATTATGGCTGCTTGCCCTACAGTTGGCAGACAGCCG  
TTTGTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAAATGTGGAGTCTCCCT  
TGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAACACATCAACCTGGAAAAATG  
CAACAAATGAATTTCACGCAGTTCTCATGGGATAGGTAAAGCTGTGCTCAGCTGT  
AGATGAAATGTTGTTGACCTGCAATTACATGTGTTATTCACTCCAGCAGTGTGCTCAGCTCC  
TACCTCTGTGCCAGGGCAGCATTTCATATCAAGATCAATTCCCTCTCAGCACAGCCTGGG  
AGGGGTCATTGTTCTCCCTGTCATCAGGGATCTCAGAGGCTCAAGACTGCAAGCTGCTGCC  
CAAGTCACACAGCTAGTGAAGACCAAGAGCAGCTTCACTGTTGACTCTAAGCTCAGTGTCT  
CTCCACTACCCCACACCAGCCTGGTGCACCAAAAGTGTGCTCCAAAAGGAAGGAGAATGGGAT  
TTTCTGAGGCATGCACATCTGAATTAGGTCAAACATTCTCACATCCCTCTAAAGTAAA  
CTACTGTTAGGAACAGCAGTGTCTCACAGTGTGGGAGCCGTCTTCTAATGAAGACAATGAT  
ATTGACACTGTCCTCTTGGCAGTTGCAATTAGTAACCTGAAAGGTATATGACTGAGCGTAGCA  
TACAGGTTAACCTGCAGAACAGTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCA  
AAAATCACTTAGCAGCAACTGAAGACAATTATCAACACAGTGGAGAAAATCAAACCGAGCAGGGC  
TGTGTGAAACATGGTTGAAATTGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATG  
TTTCAGGTGTCATGGACTGTTGCCACCATGTATTCACTCCAGAGTTCTTAAAGTTAAAGTTGCA  
CATGATTGTATAAGCATGCTTCTTGAGTTTAAATTATGTATAAACATAAGTTGCATTAGAA  
ATCAAGCATAAATCACTCAACTGCAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 8**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQHKL  
RSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTGQMVFSE  
TVITSGVDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMILCTRSECCGDQLCVGHC  
TKMATRGNSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDG  
ALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEVGSFMEEVROELEDLE  
RSLTEEMALGEAAAAALLGEEI

**Signal sequence:**

amino acids 1-19

**N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

**Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

**N-myristoylation site.**

amino acids 202-208, 217-223

**Amidation site.**

amino acids 140-144

## **FIGURE 9**

CGGACGCGTGGCGGACGCGTGGGGCTGTGAGAAAGTCCAATAAATACATCATGCAACCCAC  
GGCCCACCTTGTGAACTCCTCGCCAGGGCTGATGTGCGTCTTCAGGGCTACTCATCCAAAG  
GCCTAATCCAACGTTCTGTCTCAATCTGCAAATCTATGGGTCTGGGGCTTCTGGACCTT  
AACTGGGTACTGGCCCTGGCCAATGCGTCTCGCTGGAGCCTTGCCTCCTACTGGCCTT  
CCACAAGCCCCAGGACATCCCTACCTCCCTTAATCTCGCCTCATCCGACACTCCGTTACC  
ACACTGGGTCATTGGCATTGGAGCCCTACCTGACCCCTGTGCAGATAGCCCAGGTCATCTTG  
GAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGTAGCCCCTGCATGTGCTGTTT  
CAAGTGCTGCCTCTGGTGTCTGGAAAAATTATCAAGTCTAAACCGCAATGCATACATCATGA  
TCGCCATCTACGGGAAGAATTCTGTCTCAGCCAAAATGCGTCATGCTACTCATGCGAAC  
ATTGTCAGGGTGGTGTCTGGACAAAGTCACAGACCTGCTGCTGTCTTGGGAAAGCTGCTGGT  
GGTCGGAGGCGTGGGGCTCTGCTCTTCTTCTCCGGTCGATCCGGGGCTGGTAAAG  
ACTTTAAGAGCCCCCACCTCAACTATTACTGGCTGCCATCATGACCTCCATCTGGGGCTAT  
GTCATGCCAGCGGCTCTCAGCGTGTTGGCATGTGTGGACACGCTCTCCCTGCTTCT  
GGAAGACCTGGAGCGGAACAACGGCTCCCTGGACCGCCCTACTACATGTCCAAGAGCCTCTAA  
AGATTCTGGCAAGAAGAACGAGGCGCCCCGGACAACAAGAAGAGGAAGACTGACAGCTCCGG  
CCCTGATCCAGGACTGCACCCCCACCCCAACGGTCCAGCCATCCAACCTCATTGCCTTACAGGT  
CTCCATTGTGGTAAAAAAAGGTTTAGGCCAGGCGGCTACGCCGTGATCGCTGTAATCCAACACT  
TTGAGAGGCTGAGGCGGCGGGCGGATCACCTGAGTCAGGAGTTCGAGACCAGCCTGCCAACATGGTG  
AAACCTCCGTCTCTATTAAAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCACTCC  
GCTACTCGGGAGGCTGAGGCAGGGAGAATCGCTGAACCCGGAGGCAGAGGTTGCAGTGAGCCGA  
GATCGGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAAACAAA  
AAGATTTATTAAAGATATTTGTTAACTC

## **FIGURE 10**

RTRGRTRGGCEKVPINTSCNPTAHVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLFWTL  
NWVLALGQCVLAGAFASFYWAFHKPQDIPFPLISAFIRTLRYHTGSLAFGALILTLVQIARVIL  
EYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLRNAYIMIAIYGKNFCVSAKNAFMLLMRN  
IVRVVVLVDKVTDLFFFGLVVGVGVLSSFFSGRIPGLGKDFKSPHLNYYWLPIMTSILGAY  
VIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYYMSKSLKILGKKNEAPPDNKKRKK

**Important features:**

**Transmembrane domains:**

amino acids 57-80 (type II), 110-126, 215-231, 254-274

**N-glycosylation sites.**

amino acids 16-20, 27-31, 289-293

**Hypothetical YBR002c family proteins.**

amino acids 276-288

**Ammonium transporters proteins.**

amino acids 204-231

**N-myristoylation sites.**

amino acids 60-66, 78-84

**Amidation site.**

amino acids 306-310

## **FIGURE 11**

CCCCCGCGCCCGGCCGGCGCCGGCGCCGAAGCGGGAGCCACCGCC**ATGGGGCCTGCCTGGAGCCTGC**  
TCCCTGCTCAGCTGCGCTCTGCCTCTGCGCTCTGCCCTGATCTGTGCAGCTGCTGCCCGC  
CAGCCGCAACTCCACCGTGAGCCGCTCATCTCAGTTCTTCTCTTCCGGGTGCTGGTGTCCA  
TCATTATGCTGAGCCGGCGTGAGAGTCAGCTACAAGCTGCCCTGGGTGTGAGGAGGGGCC  
GGGATCCCCACCGTCTGCAGGGCACATCGACTGTGGCTCCCTGCTGGCTACCGCGCTGTCTACCG  
CATGTGCTCGCCACGGCGGCTCTTCTTACCCCTGCTCATGCTTGCGTGAAGCAGCA  
GCCGGGACCCCCGGGCTGCCATCCAGAATGGTTTGGTCTTAAGTCCGTATCCTGGTGGCCTC  
ACCGTGGGTGCCTTACATCCCTGACGGCTCTTACCAACATCTGGTCTACTTCGGCGTGTGG  
CTCCTTCTCTTACATCCTCATCCAGCTGGTGTGCTCATCGACTTGCACACTCTGGAACCGAGCGGT  
GGCTGGGCAAGGCCGAGGAGTGGGATTCCCGTGCCTGGTACGCAGGCCCTTCTTCACTCTCCTC  
TTCTACTTGCTGTCGATCGCGGCCGTGGCGCTGATGTTCATGTAACACTGAGCCCAGCGCTGCCA  
CGAGGGCAAGGTCTTCATCAGCCTCACCTCACCTCTGTGTCTGCGTGTCCATGCTGCTGTCTGC  
CCAAGGTCCAGGACGCCAGCCCAACTGGGTCTGCTGCAGGCCCTGGTCATCACCTCACCATG  
TTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAACCCAGCT  
GGGCAACGAGACAGTTGGCAGGCCCGAGGGCTATGAGACCCAGTGGTGGGATGCCCGAGCATTG  
TGGGCCATCATCTCCCTCTGTCACCCCTTTCATCAGTCTGCGCTCTCAGACCACGGCAGGTG  
AACAGCCTGATGCAGACCGAGGAGTCCCACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGT  
GGCAGCCTGTGAGGCCGGGCTTGAACAGAGCAGGACGGCGTCACCTACAGCTACTCTTCTCC  
ACTTCTGCCTGGTGTGGCTACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCGGTGAG  
ACCCGGAAGATGATCAGCACGGACCCGCGCTGTGGGTGAAGATCTGTGCCAGTGGCAGGGCTGCT  
CCTCTACCTGTGGACCCCTGGTAGCCCCACTCCTCTGCGCAACCGCAGCTCAGCT**AGCTGAGG**CAGCCTCA  
CAGCCTGCCATCTGGTGCCTCTGCCACCTGGTGCCTCTGGCTCGGTGACAGCCAACCTGCCCTC  
CCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCAGCTCCAGGACCTGCCCTGAGCCGGC  
CTTCTAGTCGTAGTGCCTCAGGGTCCGAGGAGCATCAGGCTCTGCAAGAGCCCCATCCCCCGCCAC  
ACCCACACGGTGGAGCTGCCCTTCCCTCCCTGGTGCCTCTGGCTGGAGAGAGCAGGGAACTCCACACAG  
AGGGCTCCCTGTCTCAGGCTCCACGGAGCGGGCTGCTGGAGAGAGCAGGGAACTCCACACAG  
TGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCAGGGACCCCTGCCCTTCTG  
GACTTCGTGCCTTACTGAGTCTAAGACTTTCTAATAAACAAAGCCAGTGCCTGTAAAAAAA

## **FIGURE 12**

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVESQL  
YKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFTLLMLCVSSSRDPRAAIQ  
NGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHAWNQRWLGKAE  
ECDSRAWYAGLFFFLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFCVCVSIAAVLPKV  
QDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGYETQWWDAPSI  
VGLIIFLLCTLFISLRSSDHRQVNLSLMQTEECPPMLDATQQQQQQVAACEGRAFDNEQDGVTYSY  
SFFHFCLVLASLHVMMTLTNWYKPGTRKMISTWTAVWVKICASWAGLLLLYLWTILVAPLLLNRD  
FS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

### **FIGURE 13**

CGGGCCAGCCTGGGCGGCCAGGAACCACCCGTTAAGGTGTCTCTTTAGGGATGGTGA  
GGTTGGAAAAAGACTCCTGTAACCCCTCCTCAGGGTAACCACCTGCCAGAAGACATGGAGAACG  
CTCTCACCGGGAGCCAGAGCTCCATGCTCTGCGCAATATCCATTCCATCAACCCCACACAA  
CTCATGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTCAGGAGGAC  
TTTCTGTTGTTGTCACCTTGACCTCTTATTGTAACATTACTGTGGATAATAGAGTTAAATG  
TGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCACTATGACTACTATTCTTCATAT  
TTTGATATATTCTCTGGCAGTTTCGATTTAAAGTGTAAACTTGCATATGCTGTGCAG  
ACTGCGCCATTGGTGGCAATAGCGTTGACAACGGCAGTGACCAGTGCCTTTACTAGCAAAG  
TGATCCTTCGAAGCTTCTCTCAAGGGCTTGGCTATGTGCTGCCATCATTCACTC  
CTTGCCTGGATTGAGACGTGGTCCTGGATTCAAAGTGTACCTCAAGAACAGAAGAAA  
CAGACTCCTGATAGTTAGGATGCTTCAGAGAGGGCAGCACTTACCTGGTGGCTTCTGATG  
GTCAGTTTATTCCCTCCTGAATCGAACAGGATCTGAAGAACGCTGAAGAAAACAGGACAGT  
GAGAAACCACTTAGAACTTGACTACTTTGTTAAATGTGAAAAACCTCACAGAAAGTC  
ATCGAGGCACAAAGAGGCAGGCAGTGGAGTCCCTGTCGACAGTAAAGTGAATGGTACGTC  
CACTGCTGGCTTATTGAACAGCTAATAAGATTATTGTAATACCTCACAAACGTTGTAC  
CATATCCATGCACATTAGTGCCTGCCTGGCTGGTAAGGTAATGTGATTCATCCTCT  
TCAGTGAGACTGAGCCTGATGTGTTAACAAATAGGTGAAAGAAAGTCTGTGCTGTATTCTAATC  
AAAAGACTTAATATATTGAAGTAACACTTTTAGTAAGCAAGATACTTTTATTCAATTCA  
AGAATGGAATTTTTGTTCATGTCAGATTATTTGTATTTCTTTAACACTCTACATT  
TCCCTGTTTTAACTCATGCACATGTGCTCTTGTACAGTTTAAAGTGTAAATAAAACTG  
ACATGTCATGTGGCTAGTTTATTCTGTTGCATTATGTGATGGCTGAAGTGTGGA  
CTTGCAAAAGGGGAAGAAAGGAATTGCGAACATGTAAAATGTCACCAGACATTGTATTATT  
TTATCATGAAATCATGTTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTGAAATGC  
ACAAAATGACTTAAACCATTCATATCATGTTCTTGCCTTCAGCCAATTCAATTAAAATGAA  
CTAAATTAAAAA

## **FIGURE 14**

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESTYEGREKKGISDVRRTFCLFVTFDLLF  
VTLLWIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLLAYAVCRLRHWWAIALT  
AVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLDFKVLPOEAEEENRLLIVQDASER  
AALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-20

**Transmembrane domains:**

amino acids 54-72, 100-118, 130-144, 146-166

**N-myristoylation sites.**

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

## **FIGURE 15**

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTGGGCCGACCCGCCAGGAAAGACTGAGG  
CCGCAGGCCCTGCCCCCGCCGCTCCCTGCGCCGCCGCCCTCCCGGACAGAACGATGTGCTCAG  
GGTCCCTCTGCTGCTGCCGCTGCTCTGCTACTGGCCCTGGGCCCTGGGTGCAGGGCTGCCAT  
CCGGCTGCCAGTGCAGCCACAGACAGTCTTCTGCACTGCCGCCAGGGGACCACGGTGCC  
CGAGACGTGCCACCCGACACGGTGGGCTGTACGTCTTGAGAACGGCATCACCAGTGCACGC  
AGGCAGCTTGGCCCTGCCGGGCTGCGACTCTGGACCTGTACAGAACAGATGCCAGCC  
TGCCCAGCGGGCTTCCAGCCACTGCCAACCTCAGAACCTGGACCTGACGCCAACAGGCTG  
CATGAAATACCAATGAGACCTCCGTGGCTGCGGCCCTCGAGGCCCTACCTGGCAAGAA  
CCGCATCCGCCACATCCAGCCTGGCTGCCCTCGACACGCTGACCGCCCTCTGGAGCTCAAGCTGC  
AGGACAACGAGCTGCCGGACTGCCCGCTGCGCTGCCGCCCTGCTGCTGCTGGACCTCAGC  
CACAAACAGCCTCTGGCCCTGGAGCCGACATCTGGACACTGCCAACGTGGAGGGCTGCC  
GGCTGGCTGGGCTGCGACAGCTGGACGAGGGCTCTCAGCCGCTGCGAACCTCCACGACC  
TGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTATCCGAGGCCTCCGGGCTGACG  
CGCCTGCCGCTGGCGCAACACCCGATTGCCAGCTGCCGGCCAGGACCTGGCGGCCCTGGC  
TGCCCTGAGGAGCTGGATGTGAGAACCTAAGCCTGAGGCCCTGCCCTGGGAGCCTCTGGGCC  
TCTTCCCCCGCCTGCCGCTGCTGGCAGCTGCCGCAACCCCTCACTGCGTGTGCCCTGAGC  
TGGTTGGCCCTGGGTGCGCAGAGCCACGTCACACTGCCAGCCCTGAGGAGACGCCGCTGCCA  
CTTCCCGCCAAGAACGCTGGCCGGCTGCTCTGGAGCTGACTACGCCGACTTGGCTGCCAG  
CCACCAACACCACAGCCACAGTGCCAACACAGGAGGCCCTGGTGGGAGGCCACAGCCTGTCT  
TCTAGCTTGGCTCTACCTGGCTAGCCCCACAGGCCGCAACTGAGGCCAGGCCCTC  
CACTGCCAACCGACTGTAGGGCTGTCCCCAGGCCAGGACTGCCACCGTCCACCTGCC  
ATGGGGCACATGCCACCTGGGACACGGCACCTGGCGTGTGCTGGCGAAGGCTTCACG  
GGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACAGGCCAGGCCCTACACAGTCAGGCC  
GCCACACGGTCCCTGACCTGGGATCGAGCGGTGAGGCCACCTCCCTGCCGTGGGCTG  
AGCGCTACCTCCAGGGAGCTCCGTGAGCTGCCACTGCCACCTGCCGTGAGTACACGGTCA  
GGCCCTGATAAGCGGTGGTGAACGCTGCCACTGCCCTGGCGTGTGCTGGCGAAGGCTTCAC  
GCTGCCGCCCCAACCCACTTACCCGCTGTGCTATGCCCTTGGGCCGGGCGGGTGGCGAGG  
GCCAGGAGGCCCTGCCGGGCAACTGCCGCTCCTCATACCCCCCAGCCGCTCACTCA  
CAGGCCGCGAGGGCACTGCCGCTCCTCATGGCGCCGCCCTGCCGCGGTGCTCCCTGCC  
GCTGGCTGCCGTGGGCAGCTACTGTGTGCCGGGGCGGGCATGGCAGCAGCGCTCAGG  
ACAAAGGGCAGGTGGGGCAGGGCTGGGGCCCTGGAACTGGAGGGAGTGAAGGTCCCCTGGAG  
CCAGGCCGAGGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGGGGTCTGAGTGTGAGGTGCC  
ACTCATGGCTTCCCAGGGCTGGCCTCCAGTCACCCCTCCACGCAAAGCCCTACATCTAAGCCA  
GAGAGAGACAGGGCAGCTGGGCCGGCTCTCAGCCAGTGAAGATGCCAGGCCCTCTGCTGCC  
ACACCAACGTAAGTCTCAGTCCAACCTGGGATGTGCAAGACAGGGCTGTGACCACAGCT  
GGGCCCTGTCCTCTGGACCTCGGTCTCCTCATCTGTGAGATGCTGTGCCAGCTGAGGCC  
CTAACGTCCCCAGAACCGAGTGCTCATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCA  
CCTGGCAGGCCGCCCCCTGCCATGTGCTGGTAACGCACTGCCCTGGGCTCTGCC  
TCCAGGCCGACCCCTGGGGCCAGTGAAGGAAGCTCCGGAAAGAGCAGAGGGAGAGCGGGTAGGC  
GGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAAAAGTGGAAAGGAGATGC  
TTAGGAACATTTTGTCTTTTAAATATATATTATAAGAGATCCTTCCATTATTCT  
GGGAAGATGTTTCAAACTCAGAGACAAGGACTTGGTTTGTAAAGACAAACGATGATGATGAA  
GGCCTTGTAAAGAAAAAATAAAGATGAAGTGTGAA

## **FIGURE 16**

MCSRVPLLLPLLLLALGPGVQGCPSCQCSQPQTVCFTARQGTTVPRDVPPDTVGLYVFENGIT  
MLDAGSFAGLPGLQQLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLRRLERLY  
LGKNRIRHIQPGAFDTLDRLLEKLQDNELRALPPLRIPRLLLLDLSHNSLLALEPGILDGTANVE  
ALRLAGLGLQQLDEGLFSRLRNLHDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDL  
AGLAALQELDVSNLSQLPGDLSGLFPRLLAARNPFCNCVCPPLSWFGPWVRESHVTLASPEE  
TRCHFPPKNAGRLLLEDYADFGCPATTTATVPTTRPVVREPTALSSSLAPTWLSPTAPATEAP  
SPPSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGTRHHACLCPEGFTGLYCESQMGQGTRSPPTP  
VTPRPPRSLTGLIEPVSPSTLRVGLQRYLQGSSVQLRSIRLTYRNLSGPDKRLVTLRLPASLAEY  
TVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAV  
LLAALAAVGAAYCVRGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSE  
CEVPLMGFPGPGLQSPHLAKPYI

**Important features:**

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 579-599

**EGF-like domain cysteine pattern signature.**

amino acids 430-442

**Leucine zipper pattern.**

amino acids 197-219, 269-291

**N-glycosylation sites.**

amino acids 101-105, 117-121, 273-277, 500-504, 528-532

**Tyrosine kinase phosphorylation sites.**

amino acids 124-131, 337-345

**N-myristoylation sites.**

amino acids 23-29, 27-33, 70-76, 142-148, 187-193, 348-354,  
594-600, 640-646

## FIGURE 17

GCAGCGCGAGGCGCGGTGGCTGAGTCGTGGCAGAGCGAAGGCACAGCTCATGCG  
GGTCGGATAGGGCTGACGCTGCTGTGCGGTGCTGAGCTTGGCTCGCGTCCGG  
ATGAAGAAGGCAGCCAGGATGAATCCTAGATTCCAAGACTACTTGACATCAGATGAGTCAGTA  
AAGGACCAACTACTGCAGGCAGAGTAGTTGCTGGTCAAATATTCTGATTCAAAGAAATCTGA  
ATTAGAATCCTCTATTCAAGAAGAGGAAGACAGCCTCAAGAGCCAAGAGGGGGAAAGTGTACAG  
AAGATATCAGCTTCTAGACTCCTCAAATCCAGAAAACAAGGACTATGAAGAGCCAAGAAAGTA  
CGGAAACCAGCTTGACGCCATTGAAGGCACAGCACATGGGGAGCCCTGCCACTTCCCTTCT  
TTTCCTAGATAAGGAGTATGATGAATGTACATCAGATGGAGGGAAAGATGGCAGACTGTGGTGTG  
CTACAACTATGACTACAAAGCAGATGAAAAGTGGGGCTTTGTGAAACTGAAGAAGAGGCTGCT  
AAGAGACGGCAGATGCAGGAAGCAGAAATGATGTATCAAACCTGGAAATGAAAATCTTAATGGAAG  
CAATAAGAAAAGCCAAAAAGAGAAGCATATCGGTATCTCCAAAAGGCAGCAAGCATGAACCATA  
CCAAAGCCCTGGAGAGAGTGTATGCTCTTATTGGTGATTACTGCCACAGAATATCCAG  
GCAGCGAGAGAGATGTTGAGAAGCTGACTGAGGAAGGCCTCCCAAGGGACAGACTGCTCTGG  
CTTCTGTATGCCTCTGGACTGGTGTAAATTCAAGTCAGGCAAAGGCTTGTATATTATACAT  
TTGGAGCTTGGGGCAATCTAATAGCCCACATGGTTGGTAAGTAGACTTTAGTTGAAGGCT  
AATAATATTAACATCAGAAGAATTGTGGTTATAGCGGCCACAACCTTTCACTTGTATGATC  
CAGATTGCTGTATTAAGACCAAATATTCAAGTGAACCTCCTCAAATTCTGTAAATGGATAT  
AACACATGGAATCTACATGAAATGAAAGTGGTGGAGTCCACAATTCTTAAATGATTAG  
TTGGCTGATTGCCCTAAAAAGAGAGATCTGATAAAATGGCTCTTTAAATTTCTGTAGTTG  
GAATTGTCAGAATCATTTCACATTAGATTATCATAATTAAAAATTCTTAGTTCA  
AAATTGTAAATGGTGGCTATAGAAAAACACATGAAATATTATAAAATTTGCAACATGC  
CCTAAGAATTGTTAAATTCACTGGAGTTATTGTGCAGAATGACTCCAGAGAGCTACTTCTG  
TTTTTACTTTCATGATTGGCTGTCTCCATTCTGGTCAATTGCTACTTTCTTGCTAATTGG  
AAGATTAACTCATTAAATAAAATTATGCTAAGATTAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 18**

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLDSTTLTSDESVKDHTTAGRVVAGQIFLDSEEESEL  
ESSIQEEEDSLKSQEGESVTEDISFLESPNPNKDYEEPKKVRKPALTAIEGTAHGEPCFHFPLFLDK  
EYDECTS DGDREDGRLWCATTYDYKADEKWGFCETEEEAKRRQMQEAEMMYQTGMKILNGSNKKSQKR  
EAYRYLQKAASMNHTKALERVSYALLFGDYLQPQNIQAAREMFEKLTEEGSPKGQTALGFLYASGLGVN  
SSQAKALVYYTFGALGGNLIAHMVLVSRL

**Important features:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 195-199, 217-221, 272-276

**Tyrosine kinase phosphorylation site.**

amino acids 220-228

**N-myristoylation sites.**

amino acids 120-126, 253-259, 268-274, 270-274, 285-291, 289-295

**Glycosaminoglycan attachment site.**

amino acids 267-271

**Microbodies C-terminal targeting signal.**

amino acids 299-303

**Type II fibronectin collagen-binding domain protein.**

amino acids 127-169

**Fructose-bisphosphate aldolase class-II protein.**

amino acids 101-119

## **FIGURE 19**

AATTCAAGATTTAAGCCCATTCTGCAGTGGAAATTGATGAACTAGCAAGAGGACACCATCTTCTT  
GTATTATAACAAGAAAGGAGTGTACCTATCACACACAGGGGGAAAA**ATG**CTCTTTGGGTGCTAGG  
CCTCCTAATCCTCTGGTTCTGTGGACTCGTAAGGAAAACTAAAGATTGAAGACATCACTG  
ATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCCAGAACTTTGAT  
AAAAAGGGATTCATGTAATCGCTGCCGTGACTGAATCAGGATCAACAGCTTAAAGGCAGA  
AACCTCAGAGAGACTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGAATGTCAAGAGGACTG  
CCCAGTGGGTGAAGAACCAAGTGGGGAGAAAGGTCTCTGGGTCTGATCAATAATGCTGGTGT  
CCCGCGTGTGGCTCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAA  
CCTGTTGGACTCATCAGTGTGACACTAAATATGCTCCTTGGTCAAGAAAGCTCAAGGGAGAG  
TTATTAAATGTCTCCAGTGTGGAGGTGCGCCTTGAATCGTGGAGGGGCTATACTCCATCCAAA  
TATGCAGTGGAAAGGTTCAATGACAGCTTAAGACGGGACATGAAAGCTTGGTGCACGTCTC  
ATGCATTGAACCAGGATTGTTCAAAACAAACTGGCAGATCCAGTAAAGGTAAATTGAAAAAAAC  
TCGCCATTGGGAGCAGCTGTCTCCAGACATCAAACAATATGGAGAAGGTTACATTGAAAAA  
AGTCTAGACAAACTGAAAGGCAATAATCTATGTGAACATGGACCTCTCCGGTGGTAGAGTG  
CATGGACCACGCTCTAACAGTCTTCCCTAACACTCATTATGCCGTGGAAAGATGCCAAA  
TTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTGCAGACTTTTATTGGTAAACAGAAA  
GCAGAGCTGGCTAACCCAAAGGCAGTGT**G**ACTCAGCTAACCAATGTCTCCTCAGGCTATGA  
AATTGGCCGATTTCAAGAACACATCTCCTTCAACCCATTCTTATCTGCTCCAACCTGGACT  
CATTAGATCGTGCTTATTGGATTGCAAAAGGAGTCCCACCATCGCTGGTGTATCCAGGGT  
CCCTGCTCAAGTTCTTGAAGGAGGCTGGAATGGTACATCACATAGGCAAGTCCCTGCCCT  
GTATTTAGGCTTGCCTGCTTGGTGTGATGTAAGGAAATTGAAAGACTTGCCATTCAAATGA  
TCTTACCGTGGCTGCCATGCTTATGGCCCCAGCATTACAGTAACATTGTGAATGTTAAGT  
ATCATCTCTTATCTAAATATTAAGATAAGTCAACCCAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 20**

MLFWVLGLLILCGFLWTRKGKLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIACLTESG  
STALKAETSERLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDY  
REPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDSLRRDMK  
AFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLDKLKGKNSYVNMD  
LSPVVECMDHALTSFLPKTHYAGKDAKIFWIPLSHMPAALQDFLLLQKAE LANPKAV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

## FIGURE 21

CTGAGGC GGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTGTGCTCGGCG  
CACTCGTTCCAGCACCTCAACACGGACTCGGACACCGAAGGTTTCTTCTGGGAAGTAAAA  
GGTGAAGCCAAGAACAGCATTACTGATTCCAAATGGATGATGTTGAAGTTGTTATACAATTGA  
CATTCAAGAAATATATTCCATGCTATCAGCTTTAGCTTTATAATTCTCAGGCGAAGTAAATG  
AGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAGAATGTGGTAGGTTGGTACAAATTCCGT  
CGTCATTCAAGATCAGATCATGACGTTAGAGAGAGGCTGCTTCACAAAAACTTGCAAGGAGCATT  
TTCAAAACCAAGACCTTGTCTGCTATTAAACACCAAGTATAATAACAGAAAGCTGCTCTACTC  
ATCGACTGGAACATTCTTATATAAACCTCAAAAGGACTTTACAGGGTACCTTAGTGGTT  
GCCAATCTGGGCATGCTGAACAACACTGGGTATAAAACTGTATCAGGTTCTGTATGTCACACTGG  
TTTAGCCGAGCAGTACAAACACACAGCTCTAAATTGGAGAAGAAGATGGATCCTAAAGGAGG  
TACATAAGATAAAATGAAATGTATGCTTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTG  
GAAGACAGTGAACAAGCAGTAGATAAAACTAGTAAAGGATGTAACACAGATTAAACGAGAAATTGA  
GAAAAGGAGAGGAGCACAGATTAGGCAGCAAGAGAGAAGAACATCCAAAAGACCTCAGGAGA  
ACATTTCCTTGTCAAGGCATTACGGACCTTTTCCAAATTCTGAATTCTCATTGATGTGTT  
ATGTCTTAAAAAATAGACATGTTCTAAAGTAGCTGTAACTAACCACCATCTGATGTAGT  
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCCTGAAGCTAGTCCAGCTAGTACACCAC  
AAATCATTAAGCATAAACGCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTGGTTGTTA  
GATACACAAGACAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAACGATCCAAAAT  
GAGCAGCCCAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTGGTAATATTACGGCTC  
CTACATTTGATCCCTTAACCTTACAAGGAGATTTTTATTGCTGATGGTAAAGCCAAAC  
ATTCTATTGTTTACTATGAGCTACTGCACTAAGTTCAATTGTTACTATGTTCAACATCA  
TGTGAGCTAATACAGATAACTCTTAGTGCAATTACTTCACAAAGTACTTTCAAACATCA  
GATGCTTTATTCCAAACCTTTTCACTTCAAGTTGAGCTGGGGAAAGGCTTACACAG  
ACACATTCTTGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACT  
TAGGGAAGACAAAGTCAGGAGGATTGATTGAGCTAGGAGTTAGAGACCAGCCTGGCAACGTATT  
GAGACCATGTCATTAAAAAATGAAAAGCAAGAATAGCCTTATTCAAACATGGAAA  
GAAATTATGAAAATTCTGAGTCATTAAATTCTCCTTAAGTGATACTTTTAGAAGTA  
CATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAATAATTGCAAAACATCATCT  
AAAATTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 22**

MEGESTSAVLSGFVLGALAFQHLNTSDTEGFLLGEVKGEAKNSITDSQMDDVEVVYTIDIQKYI  
PCYQLFSFYNSSGEVNEQALKKILSNVKNNVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDL  
VFLLLTPSIITESCSTHRLEHSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVGSCMSTGFSRAV  
QTHSSKFFED GSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGA  
QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKNRHVSKSSCNYNHHLDVVDNLTL  
MVEHTDipeASPASTPQIIKKALDLDDRWFQKRSRLLDTQDKRSKANTGSSNQDKASKMSSPET  
DEEIEKMKGFGEYSRSPTF

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation sites.**

amino acids 75-79, 322-326

**N-myristoylation site.**

amino acids 184-154

**Growth factor and cytokines receptors family.**

amino acids 134-150

## **FIGURE 23**

GGCACAGCCGCGCGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCGGAGCAGCGGACCAGGCCAGGGCAGCCAA  
GCAGCGCGCAGCGAACGCCGCCGCCACACCCCTCGCGTCCCGCGCCCTGCCACCCCTCCCTCCCC  
GCGTCCCCGCCCTCGCGGCCAGTCAGCTTGCCGGTTCGCTGCCCGGAAACCCCGAGGTCAACCGCCGCCCT  
GCTTCCCTGGGCCGCGCGCCCTCACGCCCTCCTCTCCCGCTGCCGCTGGCACCGGGGACCGTTGCCTGA  
CGCGAGGCCAGCTACTTTGCCCGCGTGTCTCCGCCTGCTGCCCTTCCACCAACTCCAACCTCTTCTCCC  
TCCAGCTCCACTCGCTAGTCCCCGACTCGCCAGCCCTCGGCCGCTGCCGTAGGCCGTTCCCGTCCGGTCCAAA  
GGTGGGAACCGTCCGCCCGGCCGACCATGGCACGGTTCGGCTTGCCCGCTTCTGCACCCGGCAGTGCTC  
AGGCCGCCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGAAGTGCAGCTTTACGTGTCCAAAGGCTTC  
AACAGAACGATGCCCTCCACGAGATCAACGGTATCATTGAAGATCTGCCCCAGGGTTACCTGCTGCT  
CAAGAGATGGAGGAGAAGTACAGCCTGCAAAAGTAAAGATGATTCAAAGTGTGGTCAGCGAACAGTGAATCATTG  
CAAGCTGTCTTGCTTACGTTACAAGAAGTTGATGAATTCTCAAAGAACTACTGAAAATGAGAGAAATCCCTG  
AATGATATGTTGTGAAGACATATGGCCATTATACATGCAAAATCTGAGCTATTAAAGATCTTCTGTAGAGTTG  
AACGTTACTACGTGGGGAAATGTAACCTGGAAGAAATGCTAAATGACTTCTGGGCTGCCCTGGAGCGGATG  
TTCCGCTGGTGAACCTCCAGTACCACTTACAGATGAGTATCTGGAATGTTGAGCAAGTACGGAGCAGCTGAAG  
CCCTTCGGAGATGTCCTCGCAAATTGAACTCCAGGTTACTCGTGTCTGGTACAGCCGTACTTCGCTCAAGGC  
TTAGCGGTTGCGGGAGATGTCGTGAGCAAGGTCTCCGTGGTAACCCACAGCCAGTGTACCCATGCCCTGTTGAAG  
ATGATCTACTGTCCCACTGCCGGGTCTCGTGAECTGTGAACCCATGTTACAACACTACTGCTCAAACATCATGAGAGGC  
TGTGGCCAACCAAGGGATCTGATTTGAATGGAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTA  
GAGGGTCTTCAACATTGAATCGGTATGGATCCCATCGATGTAAGATTCTGATGCTATTATGAACATGCAGGAT  
AATAGGTTCAAGTGTCTCAGAAGGTTTCCAGGGATGTTGAGCCCTCCAGCTGGACGAATTTCGCT  
TCCATCTGAAAGTGCCTCAGTGTCTCGTTCAAGACCACATCCCCGAGGAACGCCAACACAGCAGCTGGCACT  
AGTTGGACCGACTGGTTACTGATGTCAGGAGAACTGAAACAGGCCAGAAATTCTGGCTCCCTCCGAGCAAC  
GTTTGCAACGATGAGAGGATGGCTGAGGAAACGCCAATGAGGATGACTGTTGAATGGAAAGGCCAAAGCAGGTAC  
CTGTTGGCAGTGACAGGAAATGGATTAGCCAACCAGGGCAACAACCCAGAGGTCAGGTTGACACCAGCAAACAGAC  
ATACTGATCTTCGCAAATCATGGCTTCCAGTGTGACCAAGAGTGAAGAATGCAACATGGGAACGACGTG  
GACTTCTTGATATCAGTGTGAAAGTAGTGGAGAAGGAAGTGGAAAGTGGCTGTGAGTATCAGCAGTGCCTTCAGAG  
TTTGACTACAATGCCACTGACCATGCTGGGAAGAGTCCAATGAGAAAGCCGACAGTGTGCTGGTGTCCGTCTGGGCA  
CAGGCCAACCTCTCACTGTCTTGATCTGCTTCTGGTTATGCAAGAGAGAGTGGAGATAATTCTCAAACACTGAG  
AAAAAGTGTCAACAAAGTAAAGGGCACCAGTTACATGACTTCTACCATCTAGTGACTTGTCTTTAAATGAA  
TGGACAACATGTACAGTTTACTATGTTGCACTGGTTAAGAAGTGTGACTTGTGTTCTCATTGAGTTGGG  
AGGAAAAGGGACTGTGCATTGAGTTGGTCTGCTCCCCAAACCATGTTAACAGTGGCTAACAGTGTAGGTACAGAA  
CTATAGTTAGTTGTGCATTGTGATCTGCCCTGTTTCTTACAACCAAACCAAGGGTCCCTTGTGGCACGTAACATGTACGTATT  
TCTGAAATATTAATAGCTGTACAGAAGCAGGTTTATTTATCATGTTATCTTAAAGAAAAAGCCAAAAAGC  
T

## **FIGURE 24**

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDA PLHEINGDHLKICPQGST  
CCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKS LNDMFVKTYGH  
LYMQNSELFKDLFVELKRYYVGVNVLEEMLNDFWARLLERMFR LVNSQYHFTDEYLECVSKYTE  
QLKPFGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVSKVSVNPTAQCTHALLKMIYCSHC RGL  
VTVKPCNYCSNIMRGCLANQGDLDFEWNNFIDAMLVAERLEGP FNIESVMDPIDVKISDAIMN  
MQDNSVQVSQKV FQGCGPPKPLPAGRISRS ISES AFSARFRPHHPEERPTTAAGTSLDRLVTDVK  
EKLKQAKKFWSLPSNV CNDERMAAGNGNE DDCWNGKGKS RYLFAVTGNGLANQGN NPEVQV DTS  
KPDILILRQIMALRVMTSKMKNAYNGNDVFFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAG  
KSANEKADSAGV RPGAQAYLLTVFCILFLVMQREW R

**Important features:**

**Signal peptide:**

amino acids 1-22

**ATP/GTP-binding site motif A (P-loop).**

amino acids 515-524

**N-glycosylation site.**

amino acids 514-518

**Glycosaminoglycan attachment sites.**

amino acids 494-498, 498-502

**N-myristoylation sites.**

amino acids 63-69, 224-230, 276-282, 438-444, 497-503, 531-537

**Glycans proteins.**

amino acids 54-75, 105-157, 238-280, 309-346, 423-460, 468-506

## **FIGURE 25**

CTCGCCCTCAAATGGGAACGCTGGCTGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGAC  
CTGAGTCATCCCCAGGGATCAGGAGCCTCAGCAGGGAACCTCCATTATATTCTCAAGCACT  
TACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTTCCCTCCTGTTGCTGCCACTAA  
TGCTGATGTCCATGGCTCTAGCAGCCTGAATCCAGGGTGCAGAGGCCACAGGGACCGAGGC  
CAGGCTCTAGGAGATGGCTCCAGGAAGGGCCAAGAATGTGAGTGCAAAGATTGGTCCTGAG  
AGCCCCGAGAAGAAAATTATGACAGTGTCTGGCTGCCAAAGAAGCAGTGCCCCGTGATCATT  
TCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAACAAGCATTCCAGA  
GCCTGCCAGCAATTCTCAAACAATGTCAGCTAAGAAGCTTGCTCTGCCCTTGTAGGAGCTCG  
AGCGCCCACTTCCAATTAAACATTCTCAGCCAAGAACAGTGGACACACCTACCAAGACACTC  
TTCTTCTCCCACCTCACTCTCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAGCA  
TGTTTTCAAGATCATTGTTGCTCTCTAGTGTCTCTCGTAGCTTAGCCT  
GTGCCCTCCCTACCCAGGCTAGGCTTAATTACCTGAAAGATTCCAGGAACTGTAGCTTCC  
AGCTAGTGTCAATTAAACCTAAATGCAATCAGGAAACTAGCAAACAGAAGTCAATAAATATTTT  
AAATGTCAAAAAAAAAAAAAAA

## **FIGURE 26**

MKVLISLLLLPLMLMSMVSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFM  
TVSGLPKKQCPKCDHFKGKVNKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

**Important features:**

**Signal peptide:**

amino acids 1-22

**N-myristoylation sites.**

amino acids 27-33, 46-52

## **FIGURE 27**

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTCCCCAGCGGAAGCACAGCTCAG  
AGCTGGTCTGCCATGGACATCCTGGTCCCACCTCTGCAGCTGCTGGTCTGCTTACCTGCC  
CCTGCACCTCATGGCTCTGCTGGCTGCTGGCAGCCCTGTGCAAAGCTACTTCCCTACCTGA  
TGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAGCTTCAGCAG  
ATAAAGGGCTTACAGGAGCCTCCGGAAAGTGGCCTACTGGAGCTGGCTGCGGAACCGGAGC  
CAACTTCAGTTCTACCCACCAGGCTGCAGGGCACCTGCCTAGACCCAAATCCCCACTTGAGA  
AGTTCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTGTGGTGGCTCCT  
GGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGCTGCACTCTGGTGTG  
CTCTGTGCAGAGCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCCGGAGGTGTG  
TCTTTTCTGGGAGCATGTGGCAGAACCATATGAAAGCTGGGCTTCATGTGGCAGCAAGTTTC  
GAGCCCACCTGAAACACATTGGGATGGCTGCTGCCCTACCAGAGAGACCTGGAAGGATCTGA  
GAACGCCAGTTCTCGAAATCCAATGGAACGACAGCCCCCTCCCTGAAGTGGCTACCTGTTG  
GGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTCCAAGCTCCAAGGCACACTTGTCC  
TTCCCCAGCCTCCAATTAGAACAGCCACCCACCAGCCTATCTATCTTCACTGAGAGGGACCTA  
GCAGAAATGAGAGAACACATTGATGTACCACTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC  
AATCTCAACTTCAATCCGCCCTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGG  
AAACACTAGGACCCCTGTTGTATCCTCAACTGCAAGTTCTGGACTAGTCTCCCAACGTTGCCTC  
CCAATGTTGTCCTTCCCTCGTCCATGGTAAAGCTCCTCTCGCTTCCCTGAGGCTAC  
CCATGCGTCTCTAGGAACGGTACAAAAGTCATGGTGCCTGCATCCCTGCCAGCCCCCTGAC  
CCTCTCTCCCCACTACCACCTCTTCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGG  
ATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTGTCTCAAATTTTTAATAATAGACGAA  
ACCACG

## **FIGURE 28**

MDILVPPLLQLLVLLTLPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQIKGL  
TGASGKVALLELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDM  
RQLADGSMDVVVCTLVLCVQSPRKVLQEVRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPTW  
KHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLPGPHIMGKAVKQSFPSKALICSFPSL  
QLEQATHQPIYLPLRGT

**Important features:**

**Signal peptide:**

amino acids 1-23

**Leucine zipper pattern.**

amino acids 10-32

**N-myristoylation sites.**

amino acids 64-70, 78-84, 80-86, 91-97, 201-207

## **FIGURE 29**

CAATGTTGCCTATCCACCTCCCCAAGCCCCTTACCTATGCCTGCTGCTAACGCTGCTGCTGCT  
GCTGCTGCTGCTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCCCAGAAAGTCTCTCTG  
CCACTGACGCCCATCAGGGATTGGGCCTCTTCCCCCTTCCTGTGTCCTGCCTCAT  
CGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGTGGGGATGGCTA  
AGAAAGCTGGGAGATAGGAACAGAACAGGGTAGTGGGTGGCTAGGGGGCTGCCTTATTAAA  
GTGGTTTTATGATTCTTACTAATTACAAAGATATTAAGGCCCTGTTCATTAAGAAATT  
GTTCCCTTCCCTGTGTTCAATGTTGTAAAGATTGTTCTGTGTAAATATGTCTTATAATAAAC  
AGTTAAAAGCTGAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MLLLTLLLLLKGSCLEWGLVGAQKVSSATDAPIRDWAFFPPSFLCLLPHRPAMTCQAQPRG  
EGEKVGDG

**Important features:**

**Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

## **FIGURE 31**

GTTCGAATTCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAAGTT  
CCTCCAAGCAAGTCATTCCCTTATTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCT  
ATTTGCATCTGTTGATAAAATGATGTTGACACCCCTCCACCGAATTCTAAGTGAATC**ATGTCGG**  
GAAGAGATAACAATCCTTGGCTGTATCCTCGCATTAGCCTGTCTTGGCCATGATGTTACC  
TTCAGATTCATCACCAACCCCTCGGTTCACATTTCATTGGTTATTTGGGATTGTTGTT  
TGTCTGCGGTGTTTATGGTGGCTGTATTATGACTATACCAACGACCTCAGCATAGAATTGGACA  
CAGAAAGGGAAAATATGAAGTGCCTGCTGGGTTGCTATCGTATCCACAGGCATCACGGCAGTG  
CTGCTCGTCTTGATTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTCAAATCAC  
AAATAAAGCCATCAGCAGTGCTCCCTCCTGCTGTTCCAGCCACTGTGGACATTGCCATCCTCA  
TTTCTCTGGTCCCTGGGTGGCTGTGCTGAGCCTGGAACTGCAGGAGCTGCCAGGTT  
ATGGAAGGCAGGCAAGTGGAAATATAAGCCCCTTCCGGCATTGGTACATGTGGCGTACCATTT  
AATTGGCCTCATCTGGACTAGTGAATTCATCCTGCGTGCCAGCAAATGACTATAGCTGGGCAG  
TGGTTACTGTTATTCAACAGAAGTAAAAATGATCCTCTGATCATCCCATTCTCGTCTCTC  
TCCATTCTCTCTTACCATCAAGGAACCGTTGTGAAAGGGTATTAAATCTCTGTTGAG  
GATTCCGAGAACATTGTACATGACTGAAAAGAACAGCAGCATGGTGCATTGT  
CCAGGTACCTGTCGATGCTGACTGCTGTTCTGGTCTTGACAAAATACCTGCTCCATCTC  
AACCGAAATGCATATACTACAACGTCTGCTATTAAATGGACAGATTCTGTACATCAGCAAAGATGC  
ATTCAAAATCTTGTCCAAGAACACTCAAGTCACCTTACATCTATTAAACTGCTTGAGACTTCATAA  
TTTTCTAGGAAAGGTGTTAGTGGTGTGTTCACTGTTGGAGGACTCATGGCTTTAACTAC  
AATCGGGCATTCCAGGTGTGGCGAGTCCCTCTGTTATTGGTAGCTTTGGCTACTTAGTAGC  
CCATAGTTTTATCTGTGTTGAAACTGTGCTGGATGCACCTTCCCTGTGTTGCTGTTGATC  
TGGAAACAAATGATGGATCGTCAAGAACCCCTACTTATGGATCAAGAATTCTGAGTTCGTA  
AAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGA  
GGGAACAGAACCTCAGGCCATTGTGAGATAGATAACCCATTAGGTATCTGTACCTGGAAAACATT  
TCCTCTAAGAGCCATTACAGAAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTC  
TTAAAAGACCTAATAACCCATTCTCCTCAAA

## **FIGURE 32**

MSGRDTILGLCILALALSIAMMFTFRFITTLLVHIFISLVLGILFVCGVLWWLYYDYNLDSIE  
LDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISAPFLLFQPLWTFA  
ILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQOMTIA  
GAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHG  
ALSRYLFRCYCFCWFCLDKYLLHQNAYTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGD  
FIIFLGKVLVVCFTVFGGLMAFNYNRAFQWAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFA  
VDLETNDGSSEKPYFMDQEFLSFVKRNSNKLNNAQDQDKHSLRNEEGTELQAIVR

**Important features:**

**Signal peptide:**

amino acids 1-20

**Putative transmembrane domains:**

amino acids 35-54, 75-97, 126-146, 185-204, 333-350, 352-371

**N-glycosylation sites.**

amino acids 204-208, 295-299, 313-317

**N-myristoylation sites.**

amino acids 147-153, 178-184, 196-202, 296-275, 342-348

### **FIGURE 33**

## **FIGURE 34**

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAG  
CQDPKYHVGTDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWR  
ESFIVLESKPKKGVTYPSALTYSSSKPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVA  
TPPTLPRPSPSAASTTSIPRPQSVGHRSQEMDLWSTATYTSSQNRPADPGIQRQDPSGAAFQKP  
VGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFRIQKQLLADVAQALDI  
GPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRAISFVTKNFFSKANGN  
RSGAPNVVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAVCRTNG  
FYSLHVQSWFGLHKTQPLVVKRVCCTDRILACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTN  
LTKEFEISDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGWWSGGTSTGAAINFALQL  
FKKSCKPNKRKLMILITDGRSYDDVRIPAMA AHLKGVITYAIGVAWAQEELEVIATHPARDHSFF  
VDEFDNLHQYVPRIQNICTEFNSQPRN

**Important features:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 181-200

**N-glycosylation sites.**

amino acids 390-394, 520-524

**N-myristoylation sites.**

amino acids 23-29, 93-99, 115-121, 262-268, 367-373, 389-395,  
431-437, 466-472, 509-515, 570-576, 571-577, 575-581, 627-633

**Amidation site.**

amino acids 304-308

## **FIGURE 35**

CCGAGCACAGGAGATTGCCTGCCTTAGGAGGTGGCTGCCTGTGGAAAAGCTATCAAGGAAGAAATTGC  
CAAACCATGCTTTTTCTGTTTCAGAGTAGTTACAACAGATCTGAGTGTAACTTAAGCATGGAAT  
ACAGAAAACAACAAAAACTTAAGCTTAATTCTCATCTGGAATTCCACAGTTCTTAGCTCCCTGGACCC  
GGTTGACCTGTTGGCTCTCCCGCTGGCTGCTCTACACGTGGTGCTCTCCGACTACTCACCCCGAGTGA  
AAGAACCTTCGGCTCGCGTCTGAGCTGCTGTGGATGGCCTCGGCTCTGGACTGTCCCTCCGAGTA  
GGATGTCACTGAGATCCCTCAAATGGAGCCTCTGCTGTCACTCCCTGAGTTCTTGATGTGGTAC  
CTCAGCCTCCCCACTACAATGTGATAGAACCGGTGAACGGATGTACTCTATGAGTATGAGCGATT  
CAGACAAGACTTCACTCACACTCGAGAGCATTCAAACAGTCTCATCAAATCCATTCTGGTCATT  
TGGTGACCTCCCAACCCCTCAGATGAAAGCCAGGCCAGGCCATTAGAGTTACTTGGGTGAAAAAAAGTCT  
TGGTGGGATATGAGGTTCTACATTTCTTATTAGGCCAAGAGGCTGAAAGGAAGACAAAATGTTGGC  
ATTGTCCTTAGAGGATGAAACACCTCTTATGGTACATAATCCGACAAGATTAGACACATATAATA  
ACCTGACCTTGAAAACCATTATGCCATTCAAGGTGGTAACCTGAGTTTGCCCCAATGCCAAGTACGTAATG  
AAGACAGACACTGATGTTCATCAAACTGGCAATTAGTGAAGTATCTTAAACCTAAACCACTCAGA  
GAAGTTTCACAGGTATCCTCTAAATTGATAATTCTTATAGAGGTTACCAAAAAACCCATATT  
CTTACCAAGGAGTATCCTTCAAGGTGGTCCCTCCATACTGCAGTGGGTTGGTTATATAATGTCAGAG  
TTGGTGCCAAAGGATCTATGAAATGATGGTCACGTAAAACCCATCAAGTTGAAGATGTTATGTCGGAT  
CTGTTGAATTATTAAGTGAACATTCAATTCCAGAACAGACACAAATTTCTTCTATAGATCC  
ATTGGATGTCCTGCAACTGAGACGTGTATTGCAGGCCATGGCTTTCTTCAAGGAGATCATCACTTT  
TGGCAGGTATGCTAAGGAACACCACTGCCATTATTAAACTCACATTCTACAAAAGCCTAGAAGGACAG  
GATACCTTGAAAGTGTAAATAAGTAGGTAACGTGGAAATTCAAGGTTACTGAGTTATAAGCTCA  
ACACTGAACTCATGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGG  
CCCTCAAAGATGATATGTGGAGGAATTAAATATAAGGAATTGGAGGTTTGCTAAAGAAATTAGG  
ACCAACAAATTGGACATGCTTCTGTAGACTAGAATTCTAAAAGGGTTACTGAGTTATAAGCTCA  
CTAGGCTGAAAAACAAACAAATGAGTTTATTGAAACAATGTGACTCACTGAAAGGTTTGCTGTA  
TATCTTATGTGGATTACCAATTAAAAATATATGTGAGTTCTGTGTCACAAAACCTCTCACTGAAGTTATA  
CTGAACAAAATTTCACCTGTTTGTCATTATAAGTACTTCAGTAAGATGTTGCTGAGTATTACAGTTATT  
ATTATTAAATTACTTCACCTTGTGTTTAAATGTTTGACGATTCAACATAAGATAAAAGGATAG  
TGAATCATTCTTACATGCAAACATTCCAGTTACTTAACCTGATCAGTTATTATGATAACATCACTCCA  
TTAATGAAAGTCATAGGTCAATTGCAATATCAGTAATCTCTGGACTTGTAAATATTACTGTGGT  
AATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

## **FIGURE 36**

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPIYRQDFHF  
TLREHSNCNSHQNPFLVILVTSHPSDVKARQAIRVTWGEKKSSWWGYEVLTFFLLGQEAEKEDKMLA  
LSLEDEHLLYGDIIRQDFLDTYNNLTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLL  
NLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPPYCSDLGYIMSRDLVPRUYEMMGHV  
KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHGFSSKEIITFWQVMLR  
NTTCHY

**Important features:**

**Type II transmembrane domain:**

amino acids 20-39

**N-glycosylation sites.**

amino acids 72-76, 154-158, 198-202, 212-216, 326-330

**Glycosaminoglycan attachment site.**

amino acids 239-243

**Ly-6 / u-PAR domain proteins.**

amino acids 23-37

**N-myristoylation site.**

amino acids 271-277

## **FIGURE 37**

CGCTCGGGCACCGCCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGCTCACTTTCTTCAGCTCCTTCATC  
TCGTCCTGCCAACAGAGACTACACAGTCATTAATGAAGCTGCCCTGGAGCAGAGTGGAAATATCATGTCGGAGTGCCTG  
AATATGATCAGATTGAGTGCCTGCCCTGATCCACCCAGGTTGACCATCTTGAAGAAACTGCAAGAGCTGCCGAATGGCTCATGGGGGGT  
TGAGTGTGACTCTGCCCTGATCCACCCAGGTTGACCATCTTGAAGAAACTGCAAGAGCTGCCGAATGGCTCATGGGGGGT  
ACCTTGGATGACTCTATGTGAAGGGTTCTACTGTGCAGAGTGCCTGGTACGGAGGAGACTGCATGCGATGTG  
GCCAGGTTCTGCAGGCCAAAGGGTCAGATTGTTGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTCATGC  
TAAACCTGGGTTGTCATCCAACTAAGATTGTCATGTTGAGTCTGGAGTTGACTACATGTGCCAGTATGACTATGTTGAG  
GTTCGTGATGGAGACAACCGCGATGCCAGATCATCAAGCGTGTCTGTGCAACGAGCGGCCAGCTCTATCCAGAGCATAG  
GATCCTCACTCCACGTCCTCTCCACTCCGATGCCAAGAATTGACGGTTCCATGCCATTATGAGGAGATCACAGC  
ATGCTCCTCATCCCTGTTCCATGACGGCACGTCCTGACAAGGCTGGATCTACAAGTGTCCCTGCTTGGCAGGC  
TATACTGGGCAGCGCTGTGAAAATCTCTTGAAGAAAGAAACTGCTCAGACCCCTGGGGGCCAGTCATGGTACCAAGAGAAAA  
TAACAGGGGGCCCTGGGTTATCAACGGACGCCATGCTAAATTGGCACCGTGGTGTCTTCTTTGTAACAACCTCTATGT  
TCTTAGTGGCAATGAGAAAAAGACTTGGCAGCAGAATGGAGAGTGGTCAAGGAAACAGCCCATCTGCATAAAAGCCTGCCGA  
GAACCAAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTCCGATGTCAGGTTCACTCAAGGGAGACACCAATTACACCACSTAT  
ACTCAGCGGCCCTCAGCAAGCAGAAACTGCAGAGTGCCTTACCAAGAAGCCAGCCCTCCCTTGGAGATCTGCCATGG  
ATACCAACATCTGCATACCCAGCTCCACTATGATGCATCTCACCCCTTACCCGCCTGGCAGCAGCAGGAGACATGT  
CTGAGGACTGGGAAGTGGAGTGGCGGGCACCATCCTGCATCCCTATGCGGGAAAATTGAGAACATCACTGCTCCAAAGA  
CCCAAGGGTTGCGCTGGCGTGGCAGGCCATCTACAGGAGGACAGCGGGTGCATGACGGCAGCCCTACAAAGGGAGC  
GTGGTTCTAGTGCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGCTGCCACTGTGTTACTGACCTGGGAAG  
GTCACCATGATCAAGACAGCAGACCTGAAAGTTGGGAAATTCTACCGGGATGATGACGGGATGAGAACACCATCC  
AGAGCCTACAGATTCTGCTATCATTGCACTCCAACTATGACCCCATCTGCTGATGCTGACATGCCATCTGAAGCT  
CCTAGACAAGGCCGTATCAGCACCCAGTCCAGCCATCTGCCTCGCTGCCAGTCGGATCTCAGCAGTCCCTCAGGAG  
TCCCACATCACTGTGCTGGCTGGAATGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGACTGATAACATGTT  
TGGTCAGTGTGGTGGACTCGCTGCTGTGAGGAGCAGCATGAGGACCATGGCATCCAGTGTGACTGATAACATGTT  
CTGTGCCAGTGGAACCCACTGCCCTCTGATATCTGCACTGCAGAGACAGGAGGATCGCGCTGTGCTTCCCGGG  
CGAGCATCTCTGAGCCAGCGTGGCATCTGATGGACTGGTCACTGTGAGGATGATAAAACATGCAGCCACAGGCTCTCCA  
CTGCCCTCACCAAGGTGCTCTTAAAGACTGGATTGAAAGAAATGAAATGAACCATGCTCATGCACACTCTTGAGAAG  
TGTTCCTGATATCGCTGTCAGTGTGTCATTGGTGAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACCTGGCT  
GTGCCAGGGCTCTGACTTCAGGGACAAAACACTGAGTGAAGGGTGAAGTGAACCTCCATTGCTGGTAGGCTGATGCCGCTCCA  
CTACTAGGACAGCCAATTGGAAAGATGCCAGGGCTTGCAAGAAGACTAAGTTCTCAAAGAAGACCATATACAAACCTCTCCA  
CTCCACTGACCTGGGGCTCTCCCAACTTCAGTATCACGAATGCCATCAGCTTGACCCAGGGAGATCTGGGCTCATGAG  
GCCCTTGGAGGCTCTCAAGTTCTAGAGAGACTGCCTGTGGGACAGCCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCC  
TGTGTACATGCCACAGTACAGTCTGGCTTCTCCCTCCATCTCTGTAACACATTAAATAAGGGTTGGCTCT  
GAACTACAA  
AA

## **FIGURE 38**

MELGCWTQLGLTFLOLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVVGYT  
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQ  
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQII  
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSPCFHDTGCVLDKAGSYKC  
ACLAGYTQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSNE  
KRTCQONGEWSGKQPIKACREPDKISDLVRRRVLPMQVSRETPLHQLYSAAFSKQKLQSAPTK  
KPALPFGDLPGMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPCGKIENITAP  
KTQGLRWPWQAAIYRRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADL  
KVVLGKFYRDDDREKTIQSLQISAIILHPNYDPILLADIAILKLLDKARISTRVQPICLAASR  
DLSTSFAQESHITVAGWNVLADVRSPGFKNDSLRSGVSVVDSLLCEEQHEDHGPVSVTDNMFCA  
SWEPTAPS DICTAETGGIAAVSFPGRASPEPRWHLMGLVWSWSYDKTCSHRLSTAFTKVLPPFKDWI  
ERNMK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**EGF-like domain cysteine pattern signature.**

amino acids 260-272

**N-glycosylation sites.**

amino acids 96-100, 279-283, 316-320, 451-455, 614-618

**N-myristoylation sites.**

amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,  
474-480, 491-497, 638-644, 666-672

**Amidation site.**

amino acids 56-60

**Serine proteases, trypsin family.**

amino acids 489-506

**CUB domain proteins profile.**

amino acids 150-167

## FIGURE 39

GGTTCCCTACATCCTCTCATCTGAGAACATCAGAGAGCATAATCTTCTACGGGCCGTGATTATTAAACGTGGCTTAATCTGAAGGTTCTCAGTCAAATTCTTGTGATCTACTGATTGTGGGGCATGCCAAGGTTGCTTAAGGAGCTGGCTGGTTGGCCCTTGTAGCTGACAGAACGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGCTTCTGTTGCTGGCTTGCTCAGTCTGCTAAGTACATTGACAATGTGGCAACCTGCACCTCCTGTATTCAAGAACTCTGTAAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGGCGCTACAAGATGGCTGTCCAGACGGCTGTGCCAGGCCTCACAGGCCACGGCTCCCTCCCCAGAGGTTCTGCAGCTGCCACCATCTCTTAATGACAGACAGGCCCTGGCTAGACAAACCTGCCTACGTGTCTCGGCAGAGGACGGCAGCCAGCAATCAGCCAGTGGACTCTGCCGGAGCAACCGAACTAAGGCACGCCCTTGAGAGATCCACTATTAGAACAGATCATTTAAAAAAATAATCGAGCTTGAGTGTCTTCGAAAGGACAAAGAGCGGGAGTCAGTTGCCAACCATGCCGACCAGGGCAGGGAAATTCTGAAAACACCAACTGCCCTGAAGTCTTCCAAGGTTGTACCCACCTGATTCAGATGGTAAATTACACAGCATCAAGATCAATCGAGTAGATCCCAGTGAAGGCCTCTATTAGGCTGGGGAGGTAGCGAAACCCCACTGGTCCATATCATTATCCAACACATTTATCGTGTGGGGTGATGCCAGAGACAGGCCCTGGCTACTGCCAGGAGACATCATTCTAAAGGCAACGGATGGACATCAGCAATGTCCCTCAACAACTACGCGCTGTGCTGAGCAGTGGACTGTGATGCGTGAACAGAAGTCCGCAACAACTACGCGCTGTGCTCTGCCAGCCAGGGCAGCCAGGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCGAGGAGCAGCTTGAAATAAAACTGGTGCAGCAAGGTGGATGAGCCTGGGTTTCATCTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTCGATATGGCAGCCAGAAAAGTGCAGCTCATCTGATTCAAGGCTGAAAGACGTGTTACCTCGTGTGTCAGGCTGGCCAGGTTGCCAGGCAGGAGACATCTCCAAAGCCCTCCATCTACAAATTACTGTCATGAGAACGGTGGTAAATATCAAAAGACCCGGTGAATCTCTCGCATGACCGTGCAGGGGGAGCATCACATAGAGAACAGGTGACATTGTTGATGTGGATGGGTCGAACGTGACAGAGGTGAGCCGGAGATGGAAATAAAACAGGTGACATTGTTGATGTGGATGGGTCGAACGTGACAGAGGTGAGCCGGAGCATCTCTGAGGAGACTGCAGCAGCCCAGCAGCCCTGGACTCCAACACACATGGCCCCACCCAGTGAACGTGTCAGGCTGGCATGTCAGGCTGGAAATTACACCGGTGTTGTATAACTGTAAGAATATTGTATTACGAAGAAACACAGCTGGAGTCAGGCTCTGTCAGGCTGGCATATTGAGGAGTTATGAAGAACATGAAACAAACCTTTTCATCAATCATTGTTGAAGGAAACAGCAGCTGAAAGGAAACATGATGGCTGGCAAGACTGCTGAAAGAACCTTAAAGGAAGAACATTCTAACTATTGTTCTGGCTGGCACTTTTATAGAATCAATGATGGTCAGAGGAAACAGAAAAATCACAATAGGCTAAGAAGTGAACACTATATTATCTGTCAGTTTTATATTAAAGAAAGAACATTGTAAGGAAAGTGTGATATTCTCTGCTGTCATGGTAGAAGTACATCAGGAATGATACATGCTTGGCAAGACTGCTGAAAGAACCTTAAAGGAAGAACATTCTAACTATTGTTCTGGCTGGCACTTACACCTCAGAAAATATGATTCCAAAAAAATTAAACACTAGTGTGTTTCAGTGTGGAGGATTCTCATTAACACTCTACACATTGTTATATTCTATTCAATAAAAGCCCTAAACAACTAAAATGATTGATTTGTATACCCACTGAATTCAAGCTGATTAAATTTAAAGGTATATGCTGAAGTCTGCCAAGGGTACATTATGCCATTTTAATTACAGCTAAAATATTCTTTAAATGCAATTGCTGAGAACGTTGCTTCATCAAACAAAGAATAAATATTTCAGAAGTTAAA

## **FIGURE 40**

MKALLLLVLPWLSPTYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDCASLTATAPS  
PEVSAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDGRSNRTRARPFERSTIRSRSFKKINR  
ALSVLRRTKSGSAVANHADQGRENSENTTAPEVFPRLYHLIPDGEITSIKINRVDPSESLSIRLV  
GGSETPLVHIIIQHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVM  
REQKFRSRNNGQAPDAYRPRDDSFHVLINKSSPEEQLGIKLVRVDEPGVFIIFNVLDGGVAYRHG  
QLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVSRQVRQSPDIFQEAGWNSNGSWSPG  
PGERSNTPKPLHPTITCHEKVNNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVISRDGR  
IKTGDILLNVDGVELTEVSREAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPP  
SDWSPSWVMWLELPRLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDG  
RIRCGDILLAVNGRSTSGMIHACLRLLKELKGRITLTIVSWPGTFL

**Important features:**

**Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-112, 157-161, 289-293, 384-388

**Tyrosine kinase phosphorylation sites.**

amino acids 433-441, 492-500

**N-myristoylation sites.**

amino acids 51-57, 141-147, 233-239, 344-350, 423-429, 447-453,  
467-473, 603-609

## **FIGURE 41**

ACCAGGCATTGTATCTCAGTTGTCATCAAGTCGCAATCAGATTGGAAAAGCTCAACTGAAGCTT  
CTTGCCTGCACTGAAGCAGAGAGATAGATATTACACGTAATAAAAACATGGGCTCAACCTGACT  
TTCCACCTTCCTACAAATTCCGATTACTGTTGCTGACTTTGTGCTGACAGTGGTTGGGGC  
CACCAGTAACTACTCGTGGGTGCCATTCAAGAGATTCTAAAGCAAAGGAGTTCATGGCTAATTCC  
ATAAGACCTCATTGGGAAGGGAAAAACTCTGACTAATGAAGCATTCCACGAAGAAGGTAGAACTT  
GACAACGTCCCTCTGTCTCCTTACCTCAGAGGCCAGAGCAAGCTATTCAAACCAAGATCTCAC  
TTTGGAAAGAGGTACAGGCAGAAAATCCAAAGTGTCCAGAGGCCGGTATGCCCTCAGGAATGTAAG  
CTTACAGAGGGTCGCCATCCTCGTCCCCACCGGAACAGAGAGAAAACACCTGATGTACCTGCTGGAA  
CATCTGCATCCCTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTATCCACCAGGCTGAAGG  
TAAAAGTTAATCGAGCCAAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGG  
ACTGCTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTACAAGTGTGAGGAG  
CATCCCAAGCATTGGTGGTGGCAGGAACAGCACTGGGTACAGGTTACGTACAGTGGATATTGG  
GGGTGTACTGCCCTAACGAGAGGAGCAGTTCAAGGTGAATGGATTCTCTAACAAACTACTGGGAT  
GGGGAGGCGAAGACGATGACCTCAGACTCAGGGTGAGCTCCAAAGAATGAAAATTCCGGCCCTG  
CCTGAAGTGGTAAATATACAATGGTCTTACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACG  
GATGAAGCTCTTACACCAAGTGTACAGACTGGGAGACAGATGGGTGAGTAGTTGTTCTTATAAAT  
TAGTATCTGTGGAACACAATCCTTATATCAACATCACAGTGGATTCTGGTTGGTGCATGACCC  
TGGATCTTGGTGTATTTGGAAAGAAGTATTCTTGTGCAATAATTGGCCTAGAGACTCAA  
ATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGAGCTGAATTTCCTTTGTATTCT  
TAGCAGAGCTCTGGTGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTAGTCATTGAT  
CATGAGGGTTAAATATTGTAATATGGATACTGAGGACTTTATATAAAAGGATGACTCAAAGGATAA  
AATGAACGCTATTGAGGACTCTGGTGAGGAGATTATTAAATTGAGTAATATATTATGGGAT  
AAAAGGCCACAGGAAATAAGACTGCTGAATGTCAGAGAGAACCCAGAGTTGTTCTCGCCAAGGTAGAA  
AGGTACGAAGATAACAATACTGTTATTCAATTCTGTACAATCATCTGTGAAGTGGTGGTGTCAAGGT  
GAGAAGGCCTCACAAGAGGGAGAAAAGGCAGCAATCAGGACACAGTGAACCTGGGAATGAAGA  
GGTAGCAGGAGGGTGGAGTGTCCGCTGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGC  
CTTCAGGGGAGGACCTGCCAGGTATGCCTCCAGTGATGCCACCAGAGAATACATTCTATTAGT  
TTTAAAGAGTTTGTAATGTTGAGGATATGAATTAGCAGTTACAAGTTACAGTTACAT  
ATTAACATAATAATATGTCTATCAAACCTCTGTAGTAAAATGTGAAAAGCAAA

## **FIGURE 42**

MGFNLTFHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLGKGKTLTN  
EASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPH  
RNREKHLMLLEHLHPFLQRQQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDV  
DLVPENDFNLKYKCEEHPKHLVGRNSTGYRLRYSGYFGGTALSREQFFKVNGFSNNYWGWGGED  
DDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSRVWRTDGLSSCSYKLV  
SVEHNPLYINITVDFWFGA

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 4-8, 220-224, 335-339

**Xylose isomerase proteins.**

amino acids 191-202

### **FIGURE 43**

## **FIGURE 44**

MALSSQIWAACLLLLL~~ASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRDTHFPI~~  
CIFCCGCCHRSKCGMCCKT

**Important features:**

**Signal peptide:**

amino acids 1-24

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 58-59

**N-myristoylation site.**

amino acids 44-50

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 1-12

## **FIGURE 45**

GTGGCTTCATTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCC  
TCATCTATATCCTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGT  
TCCGTTGGTGGGCGGTGACTTCCCCCTGAAGTCAAAGTAAAGCAAGTTGACTCTATTGTCTG  
GACCTTCAACACAACCCCTCTTGTACCACAGCCAGAAGGGGGCACTATCATAGTGACCCAAA  
ATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAGCTCAGCAAACGTAAAG  
AAGAATGACTCAGGGATCTACTATGTGGGATATACAGCTCATCAGCAGCCCTCCACCC  
GGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCTAAAGTCACCATGGGTCTGCAGAGCA  
ATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATT  
TATACCTGGAAGGCCCTGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTC  
CTGGAGATGGGAGAAAGTGAATGACCTTCATCTGCCTGCCAGGAACCTGTCAAGCAGAACT  
TCTCAAGCCCCATCCTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCATG  
GTCCTCCTGTGTCTCCTGTTGGTGCCTCCTGCTCAGTCCTTGACTGGGCTATTCTTG  
GTTTCTGAAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGTGGACATTGTCGGG  
AAACTCCTAACATATGCCCTATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAAT  
AGAACAACTCTAAAGGAAGATCCAGCAAATACGGTTACTCCACTGTGAAATACGAAAAAGAT  
GGAAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTGCCTATGAGAATGTTA  
TCTAGACAGCAGTGCACTCCCCTAAGTCTGCTCA

## **FIGURE 46**

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSGGAVTFPLSKVKQVDSIVWTFTNTPLVTIQP  
EGGTIIVTQNRNRERVDFPDGGYSLKLSKKNDSGIYYVGIYSSSLQQPSTQEYVLHVEHLSK  
PKVTMGLQSNKNGTCVTNLTCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFIG  
VARNPVSRNFSSPILARKLCEGAADDPDSSMVLCLLVPLLLFLVGLFLWFLKRERQEEYIE  
EKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIPKKMENPHSLLTMPDT  
PRLFAYENVI

**Important features:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 224-250

**Leucine zipper pattern.**

amino acids 229-251

**N-glycosylation sites.**

amino acids 98-102, 142-146, 148-152, 172-176, 176-180, 204-208,  
291-295

## **FIGURE 47**

GGCTCGAGCGTTCTGAGCCAGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGG  
ATTCAGCCCTGCTGGTCTACTGCTGTTAGGAGTAGTCTCAATGCGATACCCTCAATTGTCAGCT  
TAGTTGAGGAAGACCAATTTCCAAAACCCATCTCTGCTTGAGTGGTGGTCCCAGGAATT  
ATAGGAGCAGGTCTGATGCCATTCCAGCAACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTG  
CTGCAACAACAGAACTGGAATGTTCTTCATCATTTCAGAGTCATTGGTGCTC  
TGTATTGCATGCTGATATCCATCCAGGCTCTCTAAAGGTCCCTCATGTGTAATTCTCCAAGC  
AACAGTAATGCCAATTGTAATTTCATTGAAAAACATCAGTGACATTCCAGAACATCTCAA  
CTTGCAGAGTGGTTTCCAATGACTCTTGACCTCCTACTGGTTCAATAAACCCACCAGTAACG  
ACACCATGGCGAGTGGCTGGAGAGCATCTAGTTCCACTTCGATTCTGAAAGAAAACAAACATAGG  
CTTATCCACTCTCAGTATTTAGGTCTATTGCTTGGAAATTCTGGAGGTCTGTTGGGCT  
CAGTCAGATAGTCATCGGTTCCCTGGCTGTGTGGAGTCTAAAGCGAAGAAGTCAAATTG  
**TGTAGTTAATGGGAAATAAATGTAAGTATCAGTAGTTGAAAAAA**

## **FIGURE 48**

MTCCEGWTSCNGFSLLVLLLGVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPA  
TTMSLTARKRACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSL  
KNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHFDSEENKHRLIHFSVFLGL  
LLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

**Important features:**

**Transmembrane domains:**

amino acids 10-31 (type II), 50-72, 87-110, 191-213

**N-glycosylation sites.**

amino acids 80-84, 132-136, 148-152, 163-167

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 223-227

**N-myristylation sites.**

amino acids 22-28, 54-60, 83-89, 97-103, 216-222

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 207-218

**TNFR/NGFR family cysteine-rich region protein.**

amino acids 4-12

## **FIGURE 49**

ATCCGTTCTCGCGCTGCCAGCTCAGGTGAGCCCTGCCAAGGTGACCTCGCAGGACACTGGTGA  
AGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAG  
ATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTGAACTGTGA  
**CATGGAGAGAGT** GACCTGGCCCTCTCCTACTGGCAGGCCTGACTGCCTTGGAAAGCCAATGACC  
CATTTGCCAATAAACGATCCCTTCACTATGACTGGAAAAACCTGCAGCTGAGCGGACTGATC  
TGC GGAGGGCTCCTGGCATTGCTGGATCGCGGAGTTCTGAGTGGCAAATGCAAATACAAGAG  
CAGCCAGAACGAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTCTGCCA  
CTACTTGCT**TGAGC**ACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCAGCACC  
TCCTCCCCCTGGGAGGGCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCCCT  
TTCTGATCAGGAGGGCTTCTTATGAATTAAACTCGCCCCACCACCCCTCA

## **FIGURE 50**

MERVTLALLLAGLTALLEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKS  
SQKQHSPVPEKAIPPLITPGSATTC

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 36-59

**N-myristoylation sites.**

amino acids 41-47, 45-51, 84-90

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7.**

amino acids 54-67

## **FIGURE 51**

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGACAGGAGAGAGAAGGCTGCAGACCCAGAGGGAGGG  
AGGACAGGGAGTCGGAAGGAGGAGCACAGAGGAGGGCACAGAGACCCAGAGCAAGGGCGGCAAGG  
AGGAGACCCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGCTGGCAGAGAATGAAGTCCAG  
GGGCCCCCTGGCCTGCCCTGCTGGCCCTGCGCTGGCAGTGGGAGGCTGGCCCTGAG  
CGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCCTGGAGACGCCCTGA  
GCGAAGGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGTGGCTCTAAAGTCAGTGAG  
GCCCTGGCCAAGGGACCAGAGAACAGCTGGCACTGGAGTCAGGCAGGTTCCAGGCTTGGC  
AGCAGATGCTTGGCAACAGGGTCGGGAAGCAGCCATGCTCTGGAAACACTGGCAGGAGA  
TTGGCAGACAGGCAGAACAGATGTCATTGACACGGAGCAGATGCTGTCGCGGCTCCTGGCAGGGG  
GTGCCTGGCCACAGTGGTGCCTGGAAACTCTGGAGGCCATGGCATCTTGGCTCTCAAGGTGG  
CCTTGGAGGCCAGGGCCAGGGCAATCCTGGAGGTCTGGGACTCCGTGGTCCACGGATACCCCG  
GAAACTCAGCAGGCAGCTTGGATGAATCCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGA  
GGGCCACCAAACCTTGGGACCAACACTCAGGGAGCTGTGGCCAGCAGCTGGCTATGGTCAGTGAG  
AGCCAGCAACCAGAACATGAAGGGTCACGAATCCCCCACCATCTGGCTCAGGTGGAGGCTCCAGCA  
ACTCTGGGGAGGCAGCGCTCACAGTCGGCAGCAGTGGCAGTGGCAGCAATGGTACAACAAAC  
AATGGCAGCAGCAGTGGTGGCAGCAGCAGTGGCAGCAGCAGTGGCAGCAGTGGCAGCAG  
TGGCAGCAGTGGTGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCAGCAGTGG  
CCTCCTGGGATCCAGCACCGGCTCCTCCGGCAACCACGGTGGGAGCAGGGAGGAAATGGA  
CATAAACCCGGGTGTGAAAGCCAGGGATGAAGCCCCGGGAGCGGGGAATCTGGGATTCAAGGG  
CTTCAGAGGACAGGGAGTTCCAGCAACATGAGGGAAATAAGCAAAGAGGGCAATGCCCTTGG  
GAGGCTCTGGAGACAATTATCGGGGCAAGGGTCGAGCTGGGAGTGGAGGAGGTGACGCTGTT  
GGTGGAGTCATACTGTGAACTCTGAGACCTCTGGGATGTTAACCTTGACACTTCTGGAA  
GAATTTAAATCCAAGCTGGTTCATCAACTGGATGCCATAAACAAAGGACAGAGAAGCTCTC  
GCATCCCGTGACCCTCCAGACAAGGAGCCACCAGATTGATGGAGCCCCCACACTCCCTCTTAA  
AACACCACCCCTCATCACTAATCTCAGCCCTGGCCTTGAATAACCTTAGCTGCCCAACAAA  
AA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 52**

MKFQGPLACLLLALCLGSGEAGPLQSGEESTGNTIGEALGHGLDALSEGVGKAIGKEAGGAAGSKVS  
EALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVP  
GHSGAWETSGGHGIFGSQGGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGPPNF  
GTNTQGAVAQPGYGSVRASNQNEGCTNPPSGSGGSSNSGGSGSQSGSSGSGSNGDNNNGSSSGS  
SSGSSSSGSSGGSSGGSSGNSGGSRGDGSSESSWGSSTGSSSGNHGGSGGNGHKPGCEKPGNE  
ARGSGESGIQGFRGQQGVSSNMREISKEGNRLGGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGM  
FNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80,  
90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161,  
159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224,  
236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252,  
253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285,  
283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301,  
298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329,  
325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,  
387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

## **FIGURE 53**

GGAGAAGAGGTTGTGAGGACAAGCTGCTCCGACAGAAGG**TG**CGCTGCTGAGCCTGCCCTGG  
CTGGGCCCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGAGGCTCCAGTGGCT  
ACTCGCCCGCATCCTGGCTTGGACCTATGCCCTCTATAACAACTGCCGCCGGCTCCAGTGGTCC  
CACAGCCCCAAAACGGAACGGTTGGGTCACCTGGGCTGATCACTCCTACAGAGGAGGGC  
TTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCAGGGCTTACGGTATGGCTGGGTC  
CATCCCCCTCATCGTTTATGCCACCCCTGACACCATCCGGTCTATCACCAATGCCCTCAGCTGCC  
TTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGAGAAGGGATACTGCTG  
AGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCGCCCTCCATTCAACATC  
GAAGTCCTATATAACGATCTCAACAAGAGTGCAACATCATGCTTGACAAGTGGCAGCACCTGG  
CCTCAGAGGGCAGCAGTCGTCGGACATGTTGAGCACATCAGCCTCATGACCTGGACAGTCTA  
CAGAAATGCATCTTCAGCTTGACAGCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCAT  
CTTGGAGCTCAGTGCCCTGTAGAGAAAAGAAGCCAGCATACTCCAGCACATGGACTTCTGT  
ATTACCTCTCCCATGACGGCGCGCTTCCACAGGGCCTGCCGCTGGTCATGACTTCACAGAC  
GCTGTCATCCGGGAGCGCGTCGCACCCCTCCACTCAGGGTATTGATGATTTCAAAGACAA  
AGCCAAGTCCAAGAGACTTGGATTTCATTGATGTGCTTGCTGAGCAAGGATGAAGATGGAGG  
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTGGAGGCCATGACACCACG  
GCCAGTGGCCTCTCCTGGGTCTGTACAACCTTGCAGGCACCCAGAAATACCAGGAGCGCTGCC  
ACAGGAGGTGCAAGAGCTCTGAAGGACCCGATCTAAAGAGATTGAATGGGACGACCTGGCCC  
AGCTGCCCTTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATC  
TCCCAGTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCAATTACCTG  
CCTCATCGATATTATAGGGGTCATCACAAACCCAACTGTGTCGGGGATCCTGAGGTCTACGACC  
CCTTCCGCTTGACCCAGAGAACAGCAAGGGAGGTCACTCTGGCTTTATTCCCTTCTCCGCA  
GGGCCAGGAACGTGACATGGGCAAGCGTCCATGGCGAGATGAAAGTGGCCTGGCGTTGAT  
GCTGCTGCACTCCGGTCTGCCAGACCAACTGAGCCCCCGCAGGAAGCTGGAAATTGATCATGC  
GCGCCGAGGGCGGGCTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA**G****T**ACTTCTGAC  
CCATCCACCTGTTTTGCAGATTGTCATGAATAAACGGTGCTGTCAAA

## **FIGURE 54**

MSLLSLPWGLRPVAMSPWLLLLVGSWLLARILAWTYAFYNNCRLQCFQPPKRNWFWGHLG  
LITPTEEGLKDSTQMSATYSQGFTVWLGPPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKP  
WLGEGILLSGGDWKSRHRRMLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHI  
SLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYYLSHDGRRFHRAC  
RLVHDFTDAVIRERRTLPTQGIDDFFKDKAKSKTLDFIGVLLSKDEDGKALSDEDIRAEADTF  
MFGGHDTTASGLSWLYNLRHPEYQERCQEVEQELLKDRDPKEIEWDDLAQLPFLTMCVKESLR  
LHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPPEVYDPFRDPENSKGRSP  
LAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLN  
VGLQ

**Important features:**

**Transmembrane domains:**

amino acids 13-32 (type II), 77-102

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 461-471

**N-glycosylation sites.**

amino acids 112-116, 168-172

## **FIGURE 55**

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTTGA  
GCCTACTCGTTGATTGCAACTATCATGGTGCTGTGTTGCACTTACCCGTGTTCTGCCT  
TTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTGCAGTCTTGGCATTGACGTGG  
TACAGCCTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTGCCGTGTCTGC  
ATAATTCATGCCAGTTATGAAGCTTGAAGGCACTATGGACAGAAGCTGGGACAGTTT  
GTAACTATCTCGAAACCTCTGTCTTACAGACATGTGCCTTTATCTTGCAGTGTTGCTT  
GTGATTGAAACATTGAGGGTTACTTTGGAAGCAACAATACATTCTCGAACCTGAATGTCAGTA  
GCACAGGATGAGAAGTGGGTTCTGTATCTTGAGTGGAACTTCCTCATGTACCTGTTCTC  
TCTGGATGTTGTCCCACTGAATTCCCATGAAACAAACCTATTCAGCAACAGCAAAAAAAA  
AAA

## **FIGURE 56**

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCASFWWHNGLALIFCILOSLALTWYSLSFIPFAR  
DAVKKCFAVCLA

**Important features:**

**Signal peptide:**

amino acids 1-33

**Type II fibronectin collagen-binding domain protein.**

amino acids 30-72

## FIGURE 57

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGAGTGGAGCACCCAGCAGGCCAACATGCTGTCTGTGCCCTG  
TACGTGCCGTCATCGGGGAAGCCCAGACCGACTTCAGACTTGTAGTCGAAGGGCTCCGCCAGCTGAAGTCC  
ATTTCAAGCTCAGTGTCTTCATCCCCCTCCAGGAATTCTCACCTACCGCCAGTGGAAAGCAGAAAATTGTACAAGCT  
GGAGATAAGGACCTTGATGGCAGCTAGACTTTGAAGAATTGTCCATTATCTCAAGATCATGAGAAGAACGCTGAGG  
CTGGTGTAAAGATTTGGACAAAAGAATGATGGACGCATTGACGCCAGGAGATCATGCACTGCCCTGCCAGCTTG  
GGAGTCAAGATATCTGACAGCAGGCCAGAAAATTCTCAAGAGCATGGATAAAAACGCCAGATGACCATCGACTGG  
AACGAGTGGAGAGACTACCACTCCCTCACCCCTGGAAACATCCCGAGATCATCTACTTGAAGCATTCCACG  
ATCTTGATGTGGGTGAGAATCTAACGGTCCCGATGAGTTCACAGTGGAGGAGGGCAGACGGGGATGTGGTGGAGA  
CACCTGGTGGCAGGAGGTGGGGCAGGGCCGTATCCAGAACCTGCACGGCCCCCTGGACAGGCTCAAGGTCTCATG  
CAGGTCCATGCCCTCCCGCAGCAACATGGCATCTGGTGTGGCTCACTCAGATGATTGAGAAGGGAGGGCCAGG  
TCACTCTGGGGCAATGGCATCACGCTCTCAAATTGCCCTGGCAACATGCCCTATGAGCAG  
ATCAAGGCCCTTGTGGTAGTGACCAAGGAGACTCTGAGGATTCAAGAGGAGTTGGCAGGGCTTGGCAGGGCC  
ATGCCCAAGCAGCATCTACCAATGGAGGTCTGAAGACCCGGATGGCCTGCCAGAACAGGCCAGTACTCAGGA  
ATGCTGGACTGCCCAGGAGATCTGGCAGAGAGGGGGTGGCCCTTCTACAAGGCTATGCTCCCAACATGCTG  
GGCATCATCCCTATGCCCGCATCGACCTTGACTCTACAGACGCTCAAGATGCTGGCTGCAGCAGTATGCACTG  
AACAGCAGGG  
CCCCCTGGGGTAGTCAGGACCCGGATGAGGCGCAAGCCTTATTGAGGGCCTGGCAGGAGTCAAGGAGCTGGCAGCTAC  
TTCAAAACATATCTGGGGAGGGGGCTTCGGGCTGTACAGGGGGCTGGCCCCAACCTCATGAAGGTATCCCC  
GCTGTGAGCATCAGCTACGTGGTCTACGAGAACCTGAAGATCACCTGGCGTGAGTCGGGGTGACGGGGGGGG  
CGCCGGCAGTGGACTGGCTGATCCTGGGGCAGCCCTGGGGTGTGAGGCACTCTCATTGTGAATGTGCCAACACT  
AAGCTGTCAGGACGGCAACTGTGAAACCCCTAGACGCCACCCGAGGGGGGGGGAGGCTGGCAGGGCCAGGGCTT  
GTCTGCTGAGCCCGAGACCCCTCTGTGGTCTCAGGAAGACCAAGGGCTTCAAGGGTCCAGGGTCAAGGGTCA  
CTCGGGCTCACATGTGAAGGACAGGACATTCTGAGTCGGCTGCCAATAGTGAAGCTGGAGGCTGGAGGGGG  
TAGTTCTCCATTTCACCCCTTGAGCCAGCTGGCCACGGCCCTGCCCTGTGCTGCGTGATCTCCCTGTGC  
CCTCTGCTGCTGCCCTCTGCTGAGGTAAGGTGGAGGGCTACAGGCCAACATCCCACCCCTCGTCCAATCCC  
ATAATCCATGATGAAAGGTGAGGTGAGGCTGGCCCTCAGGCTGACTGGCTTCAAGGGCTTCAACCTACGATTGAC  
TGTGAAGGAAGGAAAGGATCTGGCTTGTGGTCACTGGCATCTGAGGGCTGGCTGATGGCTGGGCTCTGGG  
CTTGGGGAGCTGGCTGGCTGGCTGGCTGCACAGAAGGCAAGTGTGGGCTCATGGTCTCTGAGCT  
GGCCTGGACCCCTGTCAAGGATGGGCCACACTCAGAACCAAACACTCAGTGTCCCCACTGTGGCATGAGG  
CCAGTGTGAGGG  
ACTGG  
GAGCAGGAGCTGGCTACTGCTCAAGGTGTGGCTGAGGCTGGGGCTGGCTGGGGGGGGGGGGGGGGGGGGGGGG  
GGGACCCACATTCACTGGTCACTGGGAACCTATTATTTGTATTATTTGAACAGAGTTATGCT  
AACTATTATAGATTGTTAATTAAAGCTGTGATTTCAAGGTTATTATTTATTATGTTATGTT  
GATTGTAACCTCCCAAGGCCAGGG  
GTCCAGAGAAATTCCCTTGGGACTGGAGGGAGGAGAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
GGTGGGGAGGGCTGGCCCTGGCTTCAAGGGTTGACTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
AACCTGAGGTGAATCCAGTTATTCTCTGGCTGGAGGGTTCTTATTACTCTTCTGAATGTCAAGGCAG  
TGAGGTGCTCTCACTGTGAATTGTGGTGGGGGGGGCTGGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
CTTCTGCTGCCCTGCTAACAAATGCCGGCAACTGCCGACCTCACGGTTGCACTCCATTCCACAGAAATGACCTGA  
TGAGGAAATCTCAATAGGTGCAAAAGATGCAAAATTGTATATGAAACATATAACTGGAGTCGTAAAAAG  
CAAATTAGAAAGAATTGGACGTTAGAAGGTTCTATTAAAGCAGCTTCTAATAAAGTTGTTCAAAGCTGAAAAAA  
AA

## **FIGURE 58**

MLCLCLYVPVIGEAQTEFQYFESKGLPAELKSIFKLSVIPSQEFSTYRQWKQKIVQAGDKDLGQLDFEEFVHYLQDHEKKLRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEKILKSMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMWWRHLVAGGGAGAVSRTCTAPLDRLKVLQMVKHASRSNNMGIVGGFTQMIREGGARSLWRGNGINVLKIAPESAIKFMAYEQIKRLVGSQETLRIHERLVAGSLAGAIAQSSIYPMEVLKTRMALRKTGQYSGMILDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNSADPGVFVLLACGTMSSCQQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFGLYRGLAPNFMKVIPAVSISYVYENLKITLGVQSR

**Important features:**

**Signal peptide:**

amino acids 1-16

**Putative transmembrane domains:**

amino acids 284-304, 339-360, 376-394

**Mitochondrial energy transfer proteins signature.**

amino acids 206-215, 300-309

**N-glycosylation sites.**

amino acids 129-133, 169-173

**Elongation Factor-hand calcium-binding protein.**

amino acids 54-73, 85-104, 121-140

## FIGURE 59

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGAACCTCCCCAGCCATGGC  
TTCCCTGGGGCAGATCCTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTG  
CACTCATCATTGGCTTGGTATTCAGGGAGACACTCCATCACAGTCACTACTGTCGCCTCAGCT  
GGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTGAACCTGACATCAAACTTCTGATAT  
CGTGATACAATGGCTGAAGGAAGGTGTTAGGCTTGGTCATGAGTCAGGAAAGGAAAGATG  
AGCTGTCGGAGCAGGATGAAATGTTAGGCTTGGTCAGAGGCCGACAGCAGTGTTGCTGATCAAGTGATAGTT  
GGCAATGCCCTTTGCGGCTGAAAAACGTCAACTCACAGATGTCGGCACCTACAAATGTTATAT  
CATCACTTCTAAAGGCAAGGGAATGCTAACCTTGAGTATAAAACTGGAGCCTTCAGCATGCCGG  
AAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTGGGTGTGAGGCTCCCCGATGGTCCCC  
CAGCCCACAGTGGCTGGGATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCAAATAC  
CAGCTTGAGCTGAACTCTGAGAATGTGACCATGAAGGTTGTCTGTGCTCTACAATGTTACGA  
TCAACAAACACATACTCCTGTATGATTGAAATGACATTGCCAAAGCAACAGGGATATCAAAGTG  
ACAGAACATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTCTGTGTTG  
CTCTCTTCTTGCATCAGCTGGCACTTCTGCCTCTAGCCCTTACCTGATGCTAAATAAAT  
GTGCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTCAC  
CACCAAGATATGACCTAGTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTG  
AGCAAACAAGAGCAAGAAACAAAAAGAAGCCAAGCAGAAGGCTCCAATATGAACAAGATAAT  
CTATCTCAAAGACATATTAGAAGTGGAAAATAATTGATGTGAACTAGACAAGTGTGTTAAGA  
GTGATAAGTAAATGCACGTGGAGACAAGTCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGT  
CACCTGGGAGTGGAGGACAGGGATAGTCATGTTCTCTGAATTGGTATATGTC  
TGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCATCCAAACATATCCACATCTTATATCCAC  
AAATTAAGCTGTAGTATGTACCCCTAACAGCCTGCTAATTGACTGCCACTCGCAACTCAGGGCG  
GCTGCATTTAGTAATGGGTCAAATGATTCACCTTTATGATGCTCCAAAGGTGCCTTGGCTTC  
TCTTCCAAACTGACAAATGCCAAAGTTGAGAAAATGATCATAATTAGCATAAACAGAGCAGT  
CGGGGACACCGATTTATAAATAAACTGAGCACCTCTTTAAACAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 60**

MASLGQILFWSIISIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLS  
DIVIQWLKEGVLGLVHEFKEGKDELSSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKC  
YIITSKGKGNANLEYKTGAFSMPEVNVDYNASSETLRCEAPRWFPQPTVVVASQVDQGANFSEVS  
NTSFELNSENVTMKVVSVLYNVTINNTYSCMIENDIAKATGDIKTESEIKRRSHLQLLNASKASL  
CVSSFFAISWALLPLSPYIMLK

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 258-281

**N-glycosylation sites.**

amino acids 112-116, 160-164, 190-194, 196-200, 205-209, 216-220,  
220-224

**N-myristylation sites.**

amino acids 52-58, 126-132, 188-194

## **FIGURE 61**

TGACGTCAGAATCACCATGGCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAG  
CACCAAGGAGCCCTCCGGTAGCTACTACCCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGT  
GGGCTACCCCTGGTGGTTATGGGGCTGCCCCCTGGAGGGCTTATGGACCACAGCTGG  
TGGAGGGCCATGGACACCCAATCCTGGGATGTCCTCTGAACCTCCAGGAGGACCATATG  
GCGGTGCAGCTCCGGGGCCCTATGGTCAGCCACCTCAAGTCCCTACGGTGCCAGCAGCCT  
GGGTTTATGGACAGGGTGGCCCTCCAATGTGGATCCTGAGGCCTACTCCTGGTCCAGTC  
GGTGGACTCAGATCACAGTGGCTATATCTCATGAAGGAGCTAAAGCAGGCCCTGGTCAACTGCA  
ATTGGTCTTCATTCAATGATGAGACCTGCCATGATGATAAACATGTTGACAAGACCAAGTCA  
GGCCGCATCGATGTCAGGCTCTCAGCCCTGTGGAAATTCACTCCAGCAGTGGAAAGAACCTCTT  
CCAGCAGTATGACCGGGACCGCTGGCTCCATTAGCTACACAGAGCTGCAGCAACCTCTGTCCC  
AAATGGGCTACAACTGAGCCCCAGTTCAACCCAGCTCTGGTCTCCGCTACTGCCACGCTCT  
GCCAATCCTGCCATGCAGCTTGACCGCTTCATCCAGGTGTGCACCCAGCTGCAGGTGCTGACAGA  
GGCCTCCGGAGAAGGACACAGCTGACAAGGCAACATCCGCTCAGCTTGAGGACTTCGTCA  
CCATGACAGCTCTCGGATGCTATTGACCCAAACATCTGTGGAGAGTGGAGTGCACCAAGGGACCTT  
TCCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTCCTGCCCCCTAGAAGAAC  
ATTCTCCCTGCTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCCTGCATCATAGCCACCA  
AAATAGTGAGGACCGGGCTGAGGCCACACAGATAGGGCCTGATGGAGGAGAGGATAGAAGTTGA  
ATGTCCTGATGGCCATGAGCAGTTGAGTGACCCAGCTGGCACCAGGAGCAGGTCTTGTAAATGG  
AGTTAGTGCCAGTCAGCTGAGCTCCACCCCTGATGCCAGTGGTAGTGTTCATGGCTGTTACC  
GTTAGTACCTGTGTTCCCTCACCAAGGCCATCCTGTCACAGCAGCCATTCTCCAAAGTGGAAAT  
CTGACCAAGCATGAGAGAGATCTGCTATGGGACCAAGTGGCTGGATTCTGCCACACCCATAAAAT  
CCTTGTGTTAACTCTAGCTGCCTGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTGGCAT  
CTTGCCAGGCTCTGCCCTGCAGCTGGGACCCCTCACTTGCCCTGCCATGCTGCTCGGCT  
TCAGTCTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTAATTGCAATTTC  
ATTGGGGC<sub>AAA</sub>AGTCCAGTGAAATTGTAAGCTCAATAAAAGGATGAAACTCTGA

## **FIGURE 62**

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGYGGPAPGGPYGPPAGGGPYG  
HPNPGMFPSTPGGGPYGGAAPGGPYGQPPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSDH  
SGYISMKELKQALVNCNSSFNDETCLMMINMFDKTKSGRIDVYGFSAWKFIQQWKNLFQQYDR  
DRSGSISYTELQQALSQMGYNLSPOFTQLLVSRYCPRSANPAMQLDRFIQVCTQLQLTEAFREK  
DTAVQGNIRLSFEDFVTMTASRML

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 147-150

**Casein kinase II phosphorylation sites.**

amino acids 135-138, 150-153, 202-205, 271-274

**N-myristoylation sites.**

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

### **FIGURE 63**

CAGGATGAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCTGGTCTGCTTCATC  
TCCCAGGCCTCTTGGCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTCCAAAATTCGGGACC  
AACTTGCTCTAGCTCGGACAACTTCCACTGGCCCTCTAATCTGAACATCCGAGCCCGC  
TCTGGACCCCTAGGTCTAATGACTGGCAAGGGTTCCCTGAAGCTCAGCGTGCCTCCATCAGATG  
GCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCCTCCATCGTGGGGCTGCCTGCCATG  
GATTCTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGAGGACGCCCTGGGGGA  
AGCGCTGCCCTGAAGAACTCTTACCTCTCCAGTGCTGCCACAGGCCTCACCTGAGGCTTCACTCTCCACCAGGAC  
TGCCTGGGAGTCTCTCCGATGCCACAGGCCTCACCTGAGGCTTCACTCTCCACCAGGAC  
TCGGAGTCCAGACGACTGCCCTCTAATTCACTGGGAGCCGGGGAAAAATCCTTCCAAACG  
CCCTCCCTGGTCTCTCATCCACAGGGTCTGCCTGATCACCCCTGGGTACCTGAATCCAGTG  
TGTCTGGGAGGTGGAGGCCCTGGGACTGGTGGGAACGAGGCCATGCCACACCCTGAGGGA  
ATCTGGGTATCAATAATCAACCCAGGTACAGCTGGGAAATATTAATCGGTATCCAGGAGG  
CAGCTGGGAAATATTAATCGGTATCCAGGAGGAGCTGGGAAATATTAATCGGTATCCAGGAGG  
GCAGCTGGGAAATATTCTATACCCAGGTATCAATAACCCATTCCCTCTGGAGTTCTCCGC  
CCTCCTGGCTCTTGGAACATCCCAGCTGGCTCCCTAATCTCCAAGCCCTAGGGTGCAGTG  
GGGCTAGAGCAGATAGAGGGAAACCCAAACATTGGGAGTTAGAGTCTGCTCCGCCCTGCTG  
TGTGGGCTCAATCCAGGCCCTGTTAACATGTTCCAGCACTATCCCCACTTTCAAGGCTCTGG  
TGCTCATCTCCAATAAAATAAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AA

## **FIGURE 64**

MQGRVAGSCAPLGLLVCLHLPGLFARSIGVWEEKVSQNFQGTNL PQLGQPSSTGPSNSEHPQPAL  
DPRSNDLARVPLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPEDPWQMMAAAEDRLGEA  
LPEEELSYLSSAAALAPGSGPLPGESSPDATGLSPEASLLHQDSESRLPRSNSLGAGGKILSQRP  
PWSLIHRVLPDHPWGTLNPSVSWGPPPQGTGWGTRPMMPHPEGIWGGINNQPPGTWGNINRYPGGS  
WGNINRYPGGSWGNINRYPGGSWGNIHLYPGINNPFPGVLRPPGSSWNIPAGFPNPPSPRLQWG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Casein kinase II phosphorylation sites.**

amino acids 56-59, 155-158

**N-myristoylation sites.**

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263,  
259-264, 269-274, 270-275, 280-285, 281-286, 305-310

## **FIGURE 65**

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGTC  
TGGGCTGCCCTTGTCCCTCCTTGCACCTCCTGGCAGCTCACATGGAACAGGGCCGGGTATGA  
CTTGCAACTGAAGCTGAAGGAGTCTTCTGACAAATTCCCTCATGAGTCCAGCTCCTGGAA  
TTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTCAGGGACCAGCGTCACCCCTCACCATGC  
AAGATCTCAACACCATGTTGCTGCAACACATTGACAGCCATTGAAGCCTGTGTCCCTTGGCC  
GGGCTTTGGGCGGGGATGCAGGAGGCAGGCCCCGACCCCTGTCTTCAGCAGGCCCCACCCTC  
CTGAGTGGCAATAAATAAAATTGGTATGCTG

## **FIGURE 66**

MGSGPLVLLTLLGSSHGTGPGMTLQLKLESFLTNSSYESSFLELLEKLCLLLHLPSTSVTL  
HHARSQHHVVCNT

**Important features:**

**Signal peptide:**

amino acids 1-19

**N-glycosylation site.**

amino acids 37-41

**N-myristoylation sites.**

amino acids 15-21, 19-25, 60-66

## **FIGURE 67**

ACGGACCGAGGGTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCGGC  
CAGGTCCCCGTCCGAGGTGCCCTGGCCGGAGATGCGGTAGGAGGGCGAGCGCGAGAACCCCC  
TTCCTCGCGCTGCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGCTGCTCTGGCG  
CTGGGCTGCCGTTCTGCTGGCCGCTGGGGCGAGCCTGGGGCAAATACAGACCACCTCTGC  
AAATGAGAATAGCACTGTTGCCTTCATCCACCAAGCTCCAGCTCCGATGGCAACCTGCGTCCGG  
AAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTGGCTGCCTTGCTCCCTGGCTGTGGGCTG  
GCACTGTTGGTGGAAAGCTCAGGAGAACGGCAGACGGAGGGCACCTACCGGCCAGTAGCGA  
GGAGCAGTTCTCCATGCAGCCGAGGCCGGCCCTCAGGACTCCAAGGAGACGGTGCAGGGCT  
GCCTGCCCATCTAGGTCCCCTCCTGCATCTGTCTCCCTCATTGCTGTGACCTTGGGAAA  
GGCAGTGCCCTCTGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAAGAAGGTACTCAA  
AGACTCTGCCCTGAGGTCAAGAGAGGATGGGCTATTCACTTTATATTTATATAAAATTAG  
TAGTGAGATGTAaaaaaaaaaaaaaaa

## **FIGURE 68**

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSSSSDGNLRPEAITAIIVFS  
LLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

**Important features:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 56-80

**N-glycosylation site.**

amino acids 36-40

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 86-90

**Tyrosine kinase phosphorylation site.**

amino acids 86-94

**N-myristoylation sites.**

amino acids 7-13, 26-32

### **FIGURE 69**

## FIGURE 70

MGLFRGFVFLLVLCLLHQSNNTSFIKLNNGFEDIVIVIDPSVPEDEKIIEQIEDMVTTASTYLFE  
ATEKRFKKNVSIILIPENWKENPQYKRPKHENKHADIVIVAPPTLPGRDEPYTKQFTECGEKGHEY  
IHFTPDLGGKKQNEYGPPGKLGVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCAGISGRN  
RVYKCQGGSCLSRACRIDSTTKLYGKDCQFPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAP  
SLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPVFSLLKISQRIVCLVLDKSGSMGGKDRLNR  
MNQAAKHFLQLQTENGWSWGMVHFSTATIVNKLIQIKSSDERNTLMAGLPTYPLGGTSICSGIK  
YAFQVIGELHSQLDGSEVLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMSKITGG  
SHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIDSTVGKDTFFL  
ITWNSLPPSISLWDPSGTIMENFTVADATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSR  
AANSSVPPITVNAMNKDVNSFPSPMTVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGA  
GADSFKNDGVSYRYFTAYTENGRYSLKVRAGGGANTARLKLRRPLNRAAYIPGWWVNGEIEANPP  
RPEIDEQTTLLEDFTSRTASGGAFVVSQVPSLPLPDQYPPSQITDLDATVHEDKIIILTWTAPGDN  
FDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAI  
KSIDKSNLTSKVSNIAQVTLFIPQANPDDIDPTPTPTPTPDKSHNSGVNISTLVLSEIGSVVI  
VNFILESTTI

**Signal peptide:**

amino acids 1-21

**Putative transmembrane domains:**

amino acids 284-300, 617-633

**Leucine zipper pattern.**

amino acids 469-491, 476-498

**N-glycosylation site.**

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,  
628-632, 811-815, 832-836, 837-841, 852-856, 896-900

## **FIGURE 71**

CTCCCTTAGGTGGAAACCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGGGCAGGGTGA  
CAACAGGTGTCATCTTTGATCTCTGTGTGCTGCCCTCCTATTCAAGGAAAGACGCCAAGGTAAATTGACCCA  
GAGGAGCAATGATCTAGGCCACTCTCAACCTCCCTCTGAACCCCAGTTATGCCAGGATTACTAGAGAGTGTCA  
ACTCAACCAGCAAGCGGCCTTCGGCTTAACCTGTGGTGGAGGAGAAACCTTGTGGGGCTCGGTTCTTAGCA  
GTGCTCAGAAGTGAATTGCTGAGGGTGGACAGAAGAAAGGAAAGGTCCCTCTGCTGTGGCTGCACATCAGGAA  
GGCTGTGATGGGAATGAGGTTAACTTCAAGGCAACTCGTTCTAGCTATTGCTCTGCCCTGCAAGATCATCTTAA  
AGTAGAGAAGCTGCTCTGTGCTGGTAACTTCAAGGCAAGGAGCAACTCGTTCTAGAAGGAAATGGATGCAAGCAGCTC  
CGGGGGCCCAAACGGCATGCTCTCTGTGGCTAGCCAGGGAAAGCCCTCCGTGGGGCCCGGCTTGAGGGATGCC  
ACCGGTTCTGGACGCATGGCTGATTCTGA**ATGAT**GATGGTCGCCCCGGGCTCTGCGTGGATTCCCGGGTGGT  
GTTTGCTGGTGCCTCTGCTGTGCTATCTCTGCTGTACATGTGGCTGCACCCCAAAGGTGACGAGGGAGCAG  
CTGGCACTCAGGGCAGGCCAACGCCAACGGGAAGGGGTACCCAGGGCTCTCAGGAGTGGGAGGAGCAGCAC  
CGCAACTACGTGAGCAGCCATGAGGGAGATGCCACAGCTCAAGGAGGAGCTGAGGAGAGGACTGAGCAGCTCAGG  
AATGGGCAGTACCAAGCCAGGGATGCTGGCTGGACAGGAGCCAGAGGAGCCAGCTGAGCAGCTCAGGAGCAGCTC  
CTGGCCTCTGCACTCGCAGGGACAAGGCAGGGTAATGCTGGCGTCAAGCTGGCACAGAGTATGAGCAGCTG  
CCTTCGATAGCTTACTCTACAGAAGGTGACCGAGCTGGGACTGCCCCACCCGGAGGAGAACCTGTG  
AGGAAGGAAAGCAGGGATGAGTTGGGAAGGATTGAATCAGCCTGGAGACCTGAAACAATCTGCAGAGAACAGC  
CCCAATCACGGCTTACAGGGCTGATTCTAGAAGGGATCTACGGAAAGGACAAAGGGACATTGTAT  
GAGCTCACCTCAAGGGACCAAACAGCAATTCAACGGCTCATCTTATTGACCATTCAGCCCCATCATGAAA  
GTAAAAAAATGAAAGCTCAACATGGCAACACGCTTATCAATGTTATGTCGCTCTAGCAAAAGGGTGGACAAGTTC  
CGGCAGTCTAGCAGAAATTCTAGGGAGATGTCAGTGGAGGAGTCCATCACTGTTGTTTACTTGGG  
AAAGAAGAAATAATGAAAGTCAAGGAATACTTGAATCTCAAGGCTGGGGAGGATGTCACCTTACCTTCATC  
CAGCTGAATGGAGAAATTCTCGGGGAGCTGATGTTGGAGGCTCTCTGGAGGAGCAACGGTCTTCAGGAAACTTACCTTCATC  
TTTTCTGTGATGGACATCTACTTACATCTGATTCTCAATACGTGAGGCTGAATACACAGGGAGAAG  
GTATTTATCAGTTCTTCAGTCAGTACAATCTGGCATAATATACGGCACCATGATGCACTCCCTCCCTGGAA  
CAGCAGCTGGTCATAAGAAGGAAACTGGATTTGGAGAGACTTGGGATGACGTCAGTATGGTCAGAC  
TTCATCAATAGTGGTTTGTGATCTGGACATCAAGGCTGGGGAGGATGTCACCTTATGCAAGTATCTC  
CACACCAACTCATGTTGAGGAGACTTCTGGCAGGACTCTTCACCTCTGGCATGAGAAGCCTGCACTGGAG  
CTGACCCCCGACAGTACAAGATGTCAGTCAGTCAGGCTAACAGAAACAGAAAGACAAGTAGCAAAACAT**GA**ACTCCAGA  
GAAGGATGTTGGGAGACACTTTCTCTGGCAATTACTGAAAGTGGCTGAAACAGAGAAAAGACTTCCATAAA  
GGACGACAAAAGAATTGGACTGATGGGTGAGAGTGAAGGAGAACGCTGGGATCTCTGTTGGGCTTTTACAACAGA  
AATCACAATCTCGCTTGCCTGCAAAAGTAACCTGGCAGCTGAAAGTGTCTGACAAAGGCAAGTGTG  
AGATTATAAGCTTAATGGTGTGGAGGTTTGTGTTTACAATACACTGAGACCTGTTGTTGTGCTCATG  
AATATTICATGATTTAAAGAGCAGTTTGTAAAAAATTCAATTAGCATGAAAGCAAGCATATTCTCCTCATATGAATGA  
GCCTATCAGCAGGGCTAGTTCTAGGAATGCTAAATATCAGAAGGAGCAGGAGGAGATAGCTTATTATGACT  
AGTGAATGACATTAAGTAAATAAAATGGCAGAAAAGAAAAGAACATTAATCTGTCATATTCTCCAAAGAT  
TAACCAAAATACTCGCTTACCTGGTCTTAACTCTCCCTTTCTTTTACTGCTCAGACTGGTGTGATCTG  
TTTTCTCTGTGAGTTATAGTCTGCTTATTAAATTACCACTTGCAGCCTAACAGAGGACAAGTGGCCTAC  
ATTTTTATATTCTTAAGAAGATACTTGAGATGCAATTGAGAATCTTCAGTCAGTCAGCATTGAGACATAGGGAAAGGAAATGTTGACT  
CCAAGGACATGCCAAATGCTGATTCTGTCAGGCACGTAATGTCAGGCATTGAGACATAGGGAAAGGAAATGTTGACT  
AATACAGACGTACAGATACTTCTGTAAGGAGTATTTCGAAGGAGGAGCAACTGAAACACTGGAGGAAAAGAAAATGAC  
ACTTCTGCTTACAGAAAAGGAAACTCATTGAGACTGTTGATATGTCAGTACCTAAAGTCAGAAACCAATT  
CTCCTCAGAAGTAGGGACCCCTTCTACCTGGTAAATAACCAAGTATACCGTGTGAACCAAACATCTCTT  
AAAACAGGGTGTCTCTCTGGCTTCTGGCTTCCATAAGAAGGAAATGGAGAAAATATATATATATATATATTGT  
GAAAGATCAATCCATCTGCCAGAATCTAGTGGGATGGAAGTTTCTACATGTTATCCACCCAGGCCAGGGAAAG  
TAACTGAATTATTCTTAAGCAGTTCTACTCAATCACCAAGATGCTTCTGAAAATTGCAATTATTACCAATT  
CAAACATTCTTAAGAATACAGTAAACATGAGTGGTTCTTCATTGATGTTGAAATTATAGCCAGCACAG  
ATGCACTGAGCTAATTATCTCTTGTGTTAAAATGCAATTGTTGATTTGACTGGTAGTTATGAAATTAAACACAGG  
CCATGAATGGAAGGTTATTGACAGCTAATAAAATGATTGTTGATGAA

## **FIGURE 72**

MMMVRRGLLAWISRVVLLVLLCC AISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWE  
EQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDK  
AEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVRKDRDELVEAIESALETLNPA  
ENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAN  
TLINVIVPLAKRVDKFRQFMQNFR EM CIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNF  
TFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKVFYPVLFQSQY  
NPGIIYGHHDAVPPLQQQLVIKETGFWRDFGFGMT CQYRSDFINIGGF DLDIKGWGGEDVHLYR  
KYLHSNLIIVV RTPV RGLFHLWHEKRCMDEL TPEQYKMCM QSKAMNEASHGQLGMLVFRHEIEAHL  
RKQKQKTSSKKT

**Important features:**

**Signal peptide:**

amino acids 1-27

**N-glycosylation sites.**

amino acids 315-319, 324-328

**N-myristylation sites.**

amino acids 96-102, 136-142, 212-218, 311-317, 339-345, 393-399

**Amidation site.**

amino acids 377-381

## **FIGURE 73**

GAGACTGCAGAGGGAGATAAAAGAGAGAGGGCAAAGAGGGCAGCAAGAGAGTTGTCTGGGATCCA  
GAAACCCATGATAACCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACAGCAAGA  
GAAGCAGAGATAAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCACTCCTC  
CCTCCCTCTCTGCCTGCTCTAGTCCTAGTCCTCAAATTCCAGTCCCCTGCACCCCTTC  
CTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCTGGCTGCAGATGGGG  
GTCAACACTGGACGTATGAGGCCACATGGTCAGGACCATGGCCAGCCTCTTACCCGTAGTGT  
GGAAACAATGCCAGTCGCCATCGATATTCAAGACAGACAGTGTGACATTGACCCGTATTC  
TGCTCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGCCTTGGACCTGCACAACAATGCC  
ACACAGTCAACTCTCTGCCCTTACCCGTATCTGGGTGGACTTCCCCGAAAATATGTAGCT  
GCCAGCTCCACCTGCACTGGGTAGAAAGGATCCCCAGGGGGTCAGAACACAGATCAACAG  
TGAAGCCACATTGCAAGAGCTCCACATTGTACATTATGACTCTGATTCTATGACAGCTTGAGTG  
AGGCTGCTGAGAGGCCCTAGGGCTGGCTGGCATCTAATTGAGGTGGTGAGACTAAG  
AATATAGTTATGAACACATTGAGTCATTGCACTGAAGTCAGGCATAAAGATCAGAACACCTC  
AGTGCCTCCCTCAACCTAACAGAGAGCTGCTCCCCAACAGCTGGGCAGTACTCCGCTACAATG  
GCTCGCTCACAACTCCCCCTGCTACCGAGGTGTGCTGGACAGTTTTATAGAAGGTCCAG  
ATTTCAATGGAACAGCTGGAAAGCTTCAGGGGACATTGTTCTCCACAGAACAGGGAGCCCTCTAA  
GCTTCTGGTACAGAACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGCTTCTTCA  
TCCAAGCAGGATCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGAGGAATCTGGTTGGC  
TGTCTGCCTTCCTGGCTGTTATTCATTGCTAGAAAGATTGGAAGAACAGGGCTGGAAAA  
CCGAAAGAGTGTGGATGACTCCCTTCATGCCATCAGGAAGCCTCTAAATGGGGTAGGATCTGG  
CCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTCCCTGGACATCTTAGAGAGGAAT  
GGACCCAGGCTGTCATTCCAGGAAGAACTGCGAGGCCTCAGCCTCTCCAAACATGTAGGAGGAA  
ATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTGCAGGGGAAGTTGGG  
ATATAACCCCAAAGTCCCTACCCCTCACTTTATGGCCCTTCCCTAGATATACTGCGGGATCT  
CTCCTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATATATTTGGAAATTAAAG  
TTTCTGACTTT

## **FIGURE 74**

MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFPDPALQ  
PHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEAT  
FAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPP  
FNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEOLEKLQGTLFSTEEEPSKLLV  
QNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYFIARKIRKKRLENRKS  
VVFTSAQATTEA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

## **FIGURE 75**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGACGGGCAGTCCCTGTGTC  
TCTGGTGGTTGCCTAAACCTGCAAACATCACCTCTTATCCATCAACATGAAGAATGTCCCTACA  
ATGGACTCCACCAGAGGGCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTTCATCACAA  
ATTGGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGCTGACAGCTCC  
AGAGAAGTGGAAAGAGAAATCCAGAAGACCTCCTGTTCCATGCAACAAATATACTCCAATCTGA  
AGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCAGTGTGACCAACCAC  
ACGCTGGTGCTCACCTGGCTGGCGAACACTCTTACTGCGTACACGTGGAGTCCTCGTCCC  
AGGGCCCCCTGCCGTGCTAGCCTCTGAGAAGCAGTGTGCCAGGACTTGAAAGATCAATCAT  
CAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTGCCATATCTATTACCGTGTCTTT  
TCTGTGATGGGCTATTCCATCTACCGATAATCCACGTGGCAAAGAGAAACACCCAGCAAATT  
GATTTGATTTATGGAAATGAATTGACAAAAGATTCTTGTGCCTGCTGAAAAAAATCGTGATTA  
ACTTTATCACCTCAATATCTGGATGATTCTAAAATTCTCATCAGGATATGAGTTACTGGGA  
AAAAGCAGTGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGA  
GGAAGAGGAGGTGAAACATTAGGTATGCTCGCATTGATGGAATTGGACTCTGAAG  
AAAACACGGAAGGTACTTCTCACCCAGCAAGAGTCCCTCAGCAGAACAAACCCCCGGATAAA  
ACAGTCATTGAATATGAATATGATGTCAGAACCACTGACATTGTCGGGGCCTGAAGAGCAGGA  
GCTCAGTTGCAGGAGGGTGTCCACACAAGGAACATTGGAGTCGCAGGCAGCGTTGGCAG  
TCCTGGGCCGCAAACGTTACAGTACTCATACACCCCTCAGCTTCAAGACTTAGACCCCTGGCG  
CAGGAGCACACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCGGTCACTGGGA  
TCCCCAAACTGGCAGGCTGTGTATTCTCGCTGTCCAGCTCGACCAGGATTAGGGCTGGCG  
AGCCTCTGAGGGGGATGGCTCGGAGAGGGTCTCTATCTAGACTCTATGAGGAGCCGGCT  
CCAGACAGGCCACCAAGGAGAAAATGAAACCTATCTCATGCAATTGCAAGGAAATGGGGTTATA  
TGTGCAGATGGAAAACTGATGCCAACACTCTCTTGCCTTGTGCAAACAAAGTGTGAG  
TCACCCCTTGATCCCAGCCATAAGTACCTGGGATGAAAGAAGTTTCCAGTTGTCACTG  
CTGTGAGAATTACTTATTCTCTATTCTCATAGCACGTGTGATTGGTCATGCATGTA  
GGTCTCTTAACAATGATGGTGGCCTCTGGAGTCAGGGCTGGCGTTGTTATGCAGAGAA  
AGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTAGGTGGGTGT

## **FIGURE 76**

MSYNGLHQRVFKELKLLTLCISISSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIY  
SNLKYNVSVLNTKSMRTWSQCVTNHTLVLWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLK  
DQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDDKRFFVPAEK  
IVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKHTMLGYASHLMEIFC  
DSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQEQLSLQEEVSTQGTLLSQQA  
ALAVLGPQTLQYSYTPQLQDLDPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSFDQDS  
EGCEPSEGDSLGEEGLLSRLYEEPAPDRPPGENETYLMQFMEEWGLYVQmen

**Important features:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

## **FIGURE 77**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAGGTCTGGCATCCTGCAC TTGCTGCCCTTGACAC  
CTGGGAAGATGGCCGGCCCGTGGACCTTCACCCCTCTGTGGTTGCTGGCAGCCACCTTGATC  
CAAGCCACCCCTCAGTCCCAC TGCA GTTCTCATCCTCGGCCAAAAGTCATCAAAGAAAAGCTGAC  
ACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGTGCTCAGTGCCATGC  
GGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCTGGTGAACACCGTCTGAAGCACATC  
ATCTGGCTGAAGGTCACTCACAGCTAACATCCTCCAGTCAGGTGAAGGCCCTGCCAATGACCA  
GGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAAGACCA  
TCGTGGAGTTCCACATGACGACTGAGGCCAAGGCCACCATCCGCATGGACACCAGTGCAAGTGGC  
CCCACCCGCCTGGCCTCAGTGACTGTGCCACCGCCATGGGAGCCTGCGCATCCAAC TGCTGTA  
TAAGCTCTCCTTCCTGGTGAACGCCCTAGCTAACAGGTCACTGAACCTCTAGTGCCATCCCTGC  
CCAATCTAGTGA AAAACCCAGCTGTGTCCCGTATCGAGGCTTCTCAATGGCATGTATGCAGAC  
CTCCTGCAGCTGGTGAAGGTGCCATTCCCTCAGCATTGACCGTCTGGAGTTGACCTTCTGTA  
TCCTGCCATCAAGGGTGA CACCATT CAGCTACCTGGGGCCAAGTGTGGACTCACAGGGAA  
AGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCTGGACAACATCCG  
TTCAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTCTCCAGAAGA  
TGATCAATGAAAAGGCTGCAGATAAGCTGGATCTACCCAGATCGTAAGATCCTAACTCAGGAC  
ACTCCCGAGTTTTTATAGACCAAGGCCATGCCAAGGTGCCACTGATCGTGTGGAAAGTGT  
TCCCTCCAGTGAAGGCCCTCCGCCCTTGTCAACCTGGCATCGAACGCCAGCTCGGAAGCTCAGT  
TTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTG  
ATGAACCTGGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCCA  
CTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCCAGTGTCAATTGGTGAAGG  
CCTTGGGATTCGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTGTGCTTACTCCAGCCTCC  
TTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAAGGCTGG  
GTCCCAGCTGGGAGTATGGGTGTGAGCTCTAGACCAATCCCTCTGCAATCAATAACACTTG  
CCTGTGAAAAA

## **FIGURE 78**

MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPVKIKEKLTQELKDHNATSILQQLPLLSAMREK  
PAGGIPVLGSLVNTVLKHIWLKVITANIILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVE  
FHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNL  
VKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYLGAKLDSQGKVT  
KWFNNSAASLTMPTLDNIPFSLIVSQDVVKAAVAAVLSPEEFMVLLDSVLPESAHLKSSIGLIN  
EKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEALRPLFTLGIASSEAQFYT  
KGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIHSILLPNQNGKLRSGGPVSLVKALG  
FEAAESSLTKDALVLTPASLWKSSPVSQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457

## **FIGURE 79**

GAGAGAAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGAGC  
TTCAGCCTGAAGACAAGGGAGCAGTCCTCTGAAGACGCTCTACTGAGAGGTCTGCCATGGCCTCT  
CTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTCTGGGCTTTGGGACACTGGTGCCAT  
GCTGCTCCCCAGCTGGAAAACAAGTTCTTATGCGGTGCCAGCATTGTGACAGCAGTTGGCTCT  
CCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATACCCAGTGTGACATCTATAGC  
ACCCTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGATGGTGACATCCAGTGCAAT  
CTCCTCCCTGGCCTGCATTATCTCTGTTGGGATGAGATGCACAGTCTTCTGCCAGGAATCCC  
GAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTCATCCTGGAGGCCTCCTGGGATTC  
ATTCTGTTGCCTGGAATCTCATGGGATCCTACGGGACTCTACTCACCACGTGGCCTGACAG  
CATGAAATTGAGATTGGAGAGGGCTTTACTTGGGATTATTCTCCCTGTTCTCCCTGATAG  
CTGGAATCATCCTCTGCTTTCCCTGCTCATCCAGAGAAATCGCTCCAACACTACGATGCCCTAC  
CAAGCCCAACCTCTGCCACAAGGAGCTCTCAAGGCCGGTCAACCTCCAAAGTCAGAGTGA  
GTTCAATTCCCTACAGCCTGACAGGTATGTGTGAAGAACACCAGGGCCAGAGCTGGGGGTGGCTG  
GGTCTGTAAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGT  
GTCAGAAGGTGCTGCTGAGGATAGACTGACTTGGCATTGGATTGAGCAAAGGCAGAAATGGG  
GCTAGTGTAAACAGCATGCAGGTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCC  
TCACCTTGCTGCCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCATTCCCTTAAGCCA  
GGACTCAGAGGATCCCTTGCCCTCTGGTTACCTGGACTCCATCCCCAAACCCACTAATCACA  
TCCCCACTGACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATT  
GCTGGGGATGGGAAGGAGAAGCAGTGGCTTGTGGCATTGCTTAACCTACTTCTCAAGCTTC  
CCTCCAAAGAAACTGATTGGCCTGGAACCTCCACTCTTGTATGACTCCACAGTGCCA  
GACTAATTGTCATGAACTGAAATAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATG  
CAGGATGGGAGGACAGGAAGGAGCAGCCTGGACATTAAAAATA

## **FIGURE 80**

MASLGLQLVGYILGLLGLLGTILVAMLLPSWKTSYVGASIVTAVGFSKGLWMECATHSTGITQCD  
IYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGMRCTVFCQESRAKDRVAVAGGVFFILGGL  
LGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCSSQRNRSNYY  
DAYQAQPLATRSSPRPGQPPKVKEFNSYSLTGYV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

## **FIGURE 81**

CCACCGTCCGCCTCTCCCTCTGCTGGACCTCCCTCGTCTCCATCTCTCCCTCCTTC  
CCCGCGTTCTTTCCACCTTCTCTTCCACCTTAGACCTCCCTGCCCTCCTTCC  
GCCCACCGCTGCTTCTGGCCCTCTCGACCCCGCTCTAGCAGCAGACCTCCTGGGTCTGTGG  
GTTGATCTGTGGCCCTGTGCCCTCGTGTCTTCTGCTCCCTCCGACTCCGCTCCGG  
ACCAGCGGCCTGACCCCTGGGAAAGGATGGTCCCGAGGTGAGGGTCTCTCCCTTGCTGGGA  
CTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCAGACATGTTGCTGCTTT  
CCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCTGATGT  
ACTGCCCTGCGCTGTACCTGCTCAGAGGGGCCCATGTGAGTTACCGCCTCCACTGTCCGCCT  
GTCCACTGCCCTGACGGAGCCACAGCAATGCTGCCAGCAACGGGACCATGTACCAACACGGAG  
TCCCTCTGGACTCCGGGCCCCACCAAAGTCTGCCAGCACACGGGACCATGTACCAACACGGAG  
AGATCTCAGTGCCCATGAGCTTCCCTCCGCCCTGCCAACCCAGTGTGTGGAACCTCACAC  
ACAGAGGGCCAGATCTACTGCCCTCACAAACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCC  
ACTGCCAGACTCCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGAGCAATCGATGAAGAGGACA  
GTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAG  
AGAGGCCGGGACCCAGCCCCACTGCCCTCAGGCCCTCTGAGCTTCATCCCTGCCACTT  
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGCCTGAAGGGAGAACATAAGAAAGCCT  
GTGTGCATGGCGGGAAAGACGTACTCCCACGGGGAGGTGTGGCACCCGCCCTCCGTGCCTTCGGC  
CCCTGCCCTGCATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCC  
CACCGAGTACCCCTGCCGTACCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTGCCAGAGG  
ACAAAGCAGACCCCTGCCACAGTGAGATCAGTCTACCAAGGTGTCCAAGGCACCGGGCCGGTC  
CTCGTCCACACATCGGTATCCCAAGCCCAGACAACCTGCGTCGCTTGCCTGGAACACGAGGC  
CTCGGACTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAGAGAG  
GTGAAGTACCTGCCCAAGGCCACACAGCCAGAATCTCCACTTGACTCAGATCAAGAAAGTCAG  
GAAGCAAGACTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGGCCCCACGAAGGTCACT  
GGAACGTCTCCTAGCCAGACCCCTGGAGCTGAAGGTACGCCAGTCCAGACAAAGTGACCAAG  
ACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTATTATATTAATAAAA  
TAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAA

## **FIGURE 82**

MVPEVRVLSSLLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSE  
GAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELP  
PSRLPNQCVLCSCTEGQIYCGLTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVR  
HPQDPCSSDAGRKRGPGTPAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEHKKACVHGGKTYS  
HGEVWHPAFRAFGPLCILCTCEDGRQDCQRVTCPTEYPCRHPEKVAGKCKICPEDKADPGHSE  
ISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDEETEAQRGEVPGPRPH  
SQNLPLDSDQESQEARNLPERGTALPTARWPPRRSLERLPSPDGAEGHGQSRQSDQDITKT

**Signal peptide:**

amino acids 1-25

## **FIGURE 83**

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCGCTACGCAGAGCCTCTCC  
GTGGCTTCCGCACCTTAGCATTAGGCCAGTTCCCTTCTCTAATCCATCGTCACCTCTCCTGTCA  
TCCGTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCTCTCATGCTCAGTTGGTTCTGACT  
TCCTCAAGCTGGATCAGGGCAGTGGCAGGTGTTGGCCAGAACAGCCTGTCAGGCCAGGGGGAG  
GACGCAGCATTCTCTGTTCCACCTCTACAGGGCAGGGCAGGCCATTATGCGAGATGCCACAGTAC  
CCAGTTCTCTAGCGTGGTCCACCTCTACAGGGCAGGGCAGGCCATTATGCGAGATGCCACAGTAC  
AAGGCAGGACAAAATGGTGAAGGATTCTATTGCGGAGGGGCGATCTCTGAGGCTGGAAAACATTACT  
GTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGCTTACTACCAAGAAGGCATCTGGGAGCT  
ACAGGTGTCAGCACTGGGCTCAGTCCCTCTCATTCCATCACGGGATATGTTGATAGAGACATCCAGCTAC  
TCTGTCAGTCCTCGGGCTGGTCCCCGGCCACAGCGAAGTGGAAAGGTCACAAGGACAGGATTGTC  
ACAGACTCCAGGACAAACAGAGACATGCATGGCCTGTTGATGTGGAGATCTCTGACCGTCCAAGAGAA  
CGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGGGTGGAAATCCAGGGTACAGATAG  
GAGATACCTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAAACTCTGCTGTGGCCTA  
TTTTTGGCATTGTTGACTGAAGATTCTTCTCAAATTCCAGTGGAAATCCAGGGGAACTGGACTG  
GAGAAGAAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCACTGGAGGTGACTCTGGATCCAG  
AGACGGCTCACCGAAGCTCTGCGTTCTGATCTGAAACTGTAACCCATAGAAAAGCTCCCCAGGAGGTG  
CCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTCCAAGCAGGGAAACATTA  
CTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGCTGGAGTGTGGGGATGATGTGGACAGGAGGA  
AGGAGTACGTGACTTTGTCTCCCGATCATGGGACTCTGGGACTCTGAGCTGAATGGAGAACATTGTATTC  
ACATTAATCCCGTTTATCAGCGCTTCCCCAGGACCCACCTACAAAATAGGGTCTTCTGACTA  
TGAGTGTGGGACCATCTCTTCTCAACATAAAATGACAGTCCCTTATTATACCCCTGACATGCGGTTG  
AAGGCTTATTGAGGCCCTACATTGAGTATCCGCTCTAATGAGCAAAATGGAACATCCCATAGTCATCTGC  
CCAGTCACCCAGGAATCAGAGAAAGAGGCCTCTGGCAAAGGGCTCTGCAATCCCAGAGACAACCAACAG  
TGAGTCCTCCTCACAGGCAACCACGCCCTCCCTCCCCAGGGTGAATGTAGGATGAATCACATCCCACAT  
TCTTCTTAGGGATATAAGGTCTCTCTCCAGATCCAAAGTCCCGCAGCAGCCGGCCAAGGTGGCTTCCA  
GATGAAGGGGGACTGGCCTGTCCACATGGAGTCAGGTGTCATGGCTGCCCTGAGCTGGAGGGAAAGG  
CTGACATTACATTAGTTGCTCTCACTCCATCTGGCTAAGTGTGATCTTGAATACCACCTCTCAGGTGAAG  
AACCGTCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGCTTAG  
ATCTTATTGATGACAGAGTGTATCCTAATGGTTGTCATTATATTACACTTCAGTAAAAAA

## **FIGURE 84**

MALMLSIVLSSLKLGSQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSSVVH  
LYRDGKDQPFMOMPQYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQKAIWELQ  
VSALGSVPLISITGYVDRDIQLLCQSSGWFPRPTAKWKGPGQGDLSTDRTNRDMHGLFDVEISL  
TVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLFFGIVGLKIFFSK  
FQWKIQAELDWRRKHGQAEELRDAKHAVEVTLDPEATAHPKLCVSDLKTVTHRKPQEVPHSEKRF  
TRKSVVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLSPDHGYWVRLNGEHLYFT  
LNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTCRFEGLLPRYIEYPSYNEQNGT  
PIVICPVTQESEKEASWQRASAIPETSNSSESSQATTPFLPRGEM

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

## **FIGURE 85**

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCCCT  
GCTCTGGGGAGGGAGAGGGCGGAAGGACAGACAGAACAGTAACTGCTGACGATGCAGAGTTCCGTGA  
CGGTGCAGGAAGGCCGTGTGTCCATGTGCCCTGCTCCTCTACCCCTCGCATGGCTGGATT  
TACCCCTGGCCCAGAGTAGTTCATGGCTACTGGTCCGGAAAGGGGCAATACAGACCAGGATGCTCC  
AGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGAGGAGACTCGGGACCGATTCCACCTCCTTG  
GGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGAAGTGTGCGGGGAGA  
TACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGATTATAAACATACCGGCTCTGTGAA  
TGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAGGCACCCCTGGAGTCCGGCTGCC  
AGAACATCTGACCTGCTGTGCCCTGGCCTGTGAGCAGGGACACCCCTATGATCTCCTGGATA  
GGGACCTCCGTGTCCCCCTGGACCCCTCACCACCCGCTCCTCGGTGCTCACCTCATCCCACA  
GCCCCAGGACCATGGCACCAGCCTCACCTGTCAGAGGTGACCTTCCCTGGGGCCAGCGTGACCACGA  
ACAAGACCGTCCATCTCAACGTGCTCACCGCCTCAGAACTGACCATGACTGTCTCCAAGGA  
GACGGCACAGTATCCACAGTCTGGAAATGGCTCATCTGTCACTCCCAGAGGGCAGTCT  
GCGCCTGGTCTGTGCAGAGTTGATGCAGAGTGACAGCAATCCCCTGCCAGGCTGAGCTGGA  
GAGGCCTGACCCCTGTGCCCTCACAGCCCTAAACCCGGGGGTGCTGGAGCTGCCCTGGGTGCAC  
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCCTCTGGCTCTCAGCAGGTCTACCT  
GAACGTCTCCCTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGGGTGCTGGGGAGCTGGAG  
CCACAGCCCTGGTCTTGTCCCTGCGTCATCTCGTTGAGGTCTGCAGGAAGAAA  
TCGGCAAGGCCAGCAGCGGGCGTGGAGATACGGGCATAGAGGATGCAAACGCTGTCAGGGGTT  
AGCCTCTCAGGGGCCCTGACTGAACCTGGCAGAACAGACTCCCAGACCAGCCTCCCCAG  
CTTCTGCCCGCTCCTCAGGGGGAGGAGACTCCAGTATGCATCCCTCAGCTCCAGATGGTG  
AAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCCACAG  
ATGAGAAACTGCAGAGACTCACCCTGATTGAGGGATCACGGCCAGGGGAAGTCA  
GAGGCTGATTCTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATG  
TGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCC  
TCCCTTTATTTTTAACTAAAAGACAGACAAATTCCTA

## **FIGURE 86**

MLL LLL P L L W G R R E A E G Q T S K L L T M Q S S V T V Q E G L C V H V P C S F S Y P S H G W I Y P G P V V H G Y W F R E G  
A N T D Q D A P V A T N N P A R A V W E E T R D R F H L L G D P H T K N C T L S I R D A R R S D A G R Y F F R M E K G S I K W N Y  
K H H R L S V N V T A L T H R P N I L I P G T L E S G C P Q N L T C S V P W A C E Q G T P P M I S W I G T S V S P L D P S T T R S  
S V L T L I P Q P Q D H G T S L T C Q V T F P G A S V T T N K T V H L N V S Y P P Q N L T M T V F Q G D G T V S T V L G N G S S L  
S L P E G Q S L R L V C A V D A V D S N P P A R L S L S W R G L T L C P S Q P S N P G V L E L P W V H L R D A A E F T C R A Q N P  
L G S Q Q V Y L N V S L Q S K A T S G V T Q G V V G G A G A T A L V F L S F C V I F V V V R S C R K K S A R P A A G V G D T G I E  
D A N A V R G S A S Q G P L T E P W A E D S P P D Q P P P A S A R S S V G E G E L Q Y A S L S F Q M V K P W D S R G Q E A T D T E  
Y S E I K I H R

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

## **FIGURE 87**

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGAGTGGAGGGAGGTGAAGGAGCTCTGTAC  
CCAAGGAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTC  
TCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAAACTTACTTCAGGAATGGACCTGT  
TCTTCGTCATCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCCTAGTGCATTGA  
TGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTCTGTGACATGACCTCTG  
GGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATGCGTGGGAAGTGCACGGTG  
GGCGATCGCTGGTCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGACGGCAACTGGC  
CAACTACAACACCTTGGATCTGCAGAGGCCACGAGCGATGACTACAAGAACCTGGCTACT  
ACGACATCCAGGCCAAGGACCTGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGG  
AGAAACAGCTCCCTGCTGAGGTACCGCACGGACACTGGCTCCTCCAGACACTGGACATAATCT  
GTTTGGCATCTACCAAGAAATATCCAGTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGCC  
CGGTGATCCCTGTGGCTATGATTTGGCAGGCCAGAAAACAGCATCTTATTACTCACCCAT  
GGCCAGCGGAATTCACTGCGGGATTGTTAGTTCACTGAGGTTATTAATAACGAGAGAGCAGCAA  
CGCCTTGTGTGCTGGAATGAGGTACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAG  
GATACTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTCTGGTTGATTGGAGTGGATAT  
GGAACATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCG  
TTGAGAGTTTGTGGAGGGAACCCAGACCTCTCCACCAGAGATCCAGGATGGAGAA  
CAACTTACCCAGTAGCTAGAATGTTAATGGCAGAAGAGAAAACAATAATCATATTGACTCAAGA  
AAAAAA

## **FIGURE 88**

MNQLSFLLFLIATTRGWTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVI  
YQTFCDMTSGGGGWTLVASVHENDMRGKCTVGRWSSQQGSKADYPEDGDNWANYNTFGSAEAAT  
SDDYKNPGYYDIQAKDLGIWHVPNPKSPMQHWRNSSLRRTDTGFLQTLGHNLFGIYQKYPVKYG  
EGKCWTNDNGPVIPVYDFGDAQKTASYYSPYQREFTAGFVQFRVFNNEAANALCAGMRVTGCN  
TEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSREITEAAVLLFYR

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation site.**

amino acids 163-167

**Glycosaminoglycan attachment sites.**

amino acids 74-78, 289-293

**N-myristylation sites.**

amino acids 76-82, 115-121, 124-130, 253-259, 292-298

## **FIGURE 89**

CTAGATTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTGAACCTCCAGCCTCAGAGAC  
CGCCGCCCTTGTCCCCGAGGGCATGGGCCGGTCTCAGGGCTTGTGCCCTCTCGCTTCTGACG  
CTCCTGGCGCATCTGGTGGTCATCACCTTATTCTGGTCCCAGGACAGAACATACAGGCCTG  
CCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCT  
CTGTCACCCCTGGCCTCTTGAGTGGAGCTGGCCGGTTCCCTCTCAGGAGTCTCATGTTAAC  
AGCACCCAGAGCCTCATCTCATTGGGCTCACTGTAGTGCATCCGTGGCCCTGTCCTTCTCAT  
ATTCGAGCGTTGGAGGTGCACTACGTATTGGTACATTTTGCTTCTGCAGTGCCTTCCAGCTG  
TCACTGAAATGGCTTATTCGTCACCGTCTTGGCTGAAAAAGAAACCCTGATTACCTTCA  
TGACGGAACCTAAGGACGAAGCCTACAGGGCAAGGGCGCTCGTATTCCGTGAAGAAGGAAG  
GCATAGGCTTCGGTTTCCCCTCGAAACTGCTCTGCTGGAGGATATGTGTTGAAATAATTACG  
TCTTGAGTCTGGGATTATCCGATTGTATTAGTGCCTTGTAAATAAAATGTTTGTAGTAACA  
TTAAGACTTATACAGTTAGGGACAATTAAAAAAAAAA

## **FIGURE 90**

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFA  
VELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFC SALPAVTEMALFV  
TVFGLKKPF

**Transmembrane domain:**

amino acids 12-28 (type II), 51-66, 107-124

## **FIGURE 91**

CTGGGACCCGAAAAGAGAAGGGAGAGCGAGGGACGAGAGCGGAGGAGGAAGATGCAACTGAC  
TCGCTGCTGCTTCGTTCTGGTGCAGGGTAGCCTATCTGGTCACTGTGGCCAGGATGATG  
GTCCTCCGGCTCAGAGGACCTGAGCGTATGACCACGAGGCCAGCCCCGGCCGGTGCCT  
CGGAAGCGGGGCCACATCTCACCTAAGTCCGCCCATGGCAATTCCACTCTCCTAGGGCTGCT  
GGCCCCGCTGGGAGGCTTGGGCATTCTGGCAGCCCCCAACGCCGAACCACAGCCCC  
CACCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCACCTACTCCAACATCAAGACGGTG  
GCCCTGAACCTGCTCGTCACAGGGAAAGATTGGACCATGGCAATGGACCTCAGCGTCCACTT  
CCAACACAATGCCACAGGCCAGGGAAACATCTCATCAGCCTCGTCCCCCAGTAAAGCTGTAG  
AGTTCCACCAGGAACAGCAGATCTCATCGAAGCCAAGGCCCTCCAAAATCTTCAACTGCCGGATG  
GAGTGGGAGAAGGTAGAACGGGCCGGACCTCGCTTGCACCCACGACCCAGCCAAGATCTG  
CTCCCGAGACCACGCTCAGAGCTCAGCCACCTGGAGCTGCTCCAGGCCCTCAAAGTCGTCTGT  
TCTACATCGCCTTCTACAGCACGGACTATCGGCTGGTCCAGAAGGTGTGCCAGATTACAACACT  
CATAGTGATAACCCCTACTACCCATCTGGGTGACCCGGGGCAGGCCACAGAGGCCAGGGC  
TGGAAGGACAGGCCTGCCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAAGGGTTGGGCTC  
AGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGCCAGGGCAAGTCTCAAGTGGCAG  
AGAAAGGGTCCAAGTGTGGTCCAAACCTGAAGCTGTGGACTGACTAGATCACAGGAGCACTGG  
AGGAGGAGTGGCTCTGTGCAGCCTCACAGGGCTTGCCACGGGCCACAGAGAGATGCTGG  
TCCCCGAGGCCTGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAAC  
CCTTGGTTCTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTTCATCAGTGTGGACA  
GCCGTCAACTTAGGATGGATGGCTGAGAGGGCTTCTAGGAGCCAGTCAGCAGGGTGGGGTGG  
GCCAGAGGAGCTCCAGCCCTGCCAGTGGCGCCCTGAGCCCCCTGTGCTGTGAGCATGG  
CATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTTGACAGATTGACCATCTGTCTCCAGC  
CAGGCCACCCCTTCCAAAATCCCTCTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATG  
GCACACCCATCTTAAGCTAACAGACAGGAGCATTGTGGCTCCACACTAACGCCACAGCCCATC  
CGCGTGCTGTGTGTCCTCTCCACCCCAACCCCTGCTGGCTCCTGGAGCATCCATGTCCCG  
GAGAGGGTCCCTCAACAGTCAGCCTCACCTGTAGACCCGGGTTCTCCGGATCTGGATGGCG  
CGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGCCGCAGAGCATGTGCTGGATCTGTT  
TGTGTGTCGTGTGGTGGGGAGGGAGGGAAAGTCTGTGAAACCGCTGATTGCTGACTTT  
TGTGTGAAGAATCGTGTGTTCTGGAGCAGGAAATAAGCTGCCCGGGCA

## **FIGURE 92**

MQLTRCCFVFLVQGSILVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTL  
LGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNNGTF  
SVHFQHNATGQGNISISLVPPSKAVEFHQQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDP  
AKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKCPDNYHSDTPYYPSG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

## **FIGURE 93**

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTCGCTGCGCCTCATTGCCTCGGGCCTGCGCTGCC  
CTTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGCTTCTT  
CTGGTTGGTGTCTACTGATTGTCGCCCTGTTGGTTCATGGCAAGAGTCATTATTGACAACA  
AAGATGGACCAACACAGAAATATCTGCTGATCTTGGAGCGTTGTCCTGTCTATATCCAAGAA  
ATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTGAAGAGTATAAACCC  
AGGTGAGACAGCACCCCTCATGCGACTGCTGGCCTATGTTCTGGCTGGGCTTGAATCATGA  
GTGGAGTATTTCCCTTGTGAATACCCATCTGACTCCCTGGGCCAGGCACAGTGGGCATTCA  
GGAGATTCTCCTCAATTCTCCATTCACTGCTGGCATTATCTGCTGCATGT  
ATTCTGGGCATTGTATTTGATGGCTGTGAGAAGAAAAGTGGGCATCCTCTTATCGTC  
TCCTGACCCACCTGCTGGTGTCAAGCCCAGACCTTCATAAGTTCTTATTATGAAATAACCTGGCG  
TCAGCATTATAATCCTGGTGTCAAGCCCAGACCTTCATAAGTTCTTATTATGAAATAACCTGGCG  
AAGCCTGAAACTCTGCCTGCTGCCAAGACAAGAACTTCTTACAACCAGCGCTCCAGAT  
**AACCTCAGGGAACCAAGCACTCCAAACCGCAGACTACATCTTAGAGGAAGCACAAC****GTGCCT**  
TTTCTGAAAATCCCTTTCTGGTGAATTGAGAAAGAAATAAAACTATGCAGATA

## **FIGURE 94**

MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDG  
PTQKYLLIFGAFVSVYIQEMFRFAYYKLLKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGV  
FSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKW GILLIVLLT  
HLLVSAQTFI SYYGINLASAFIILVLMGTW AAGGSCRSLKLCLLCQDKNFLLYNQR SR

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

## **FIGURE 95**

AATTTTCACCAGAGTAAACTTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTCGTG  
GACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTTGTCTTAGGATCAAC  
TCGGTCATTACCACAGCTAAACCTGTTGGACTCCCTCCCACAAAACTGGCTCCGGATCAGG  
GAACACTACCAACCAACAGCAGTCAAATCAGGTCTTCCTTAAAGTCTGATACCATTAAACA  
CAGATGCTCACACTGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGGAATGACACCTGGTAC  
CCAGACCCACCCATTGACCCCTGGGAGGGTTGAATGTACAACAGCAACTGCACCCACATGTGTTAC  
CAATTTGTACACAACTTGGAGCCCAGGGCACTATCCTAAGCTCAGAGGAATGCCACAAATC  
TTCACGAGCCTCATCATCCATTCTTGTTCGGAGGCATCCTGCCACCAGTCAGGCAGGGC  
TAATCCAGATGTCCAGGATGGAAGCCTCCAGCAGGAGGAGCAGGTGTAATCCTGCCACCCAGG  
GAACCCAGCAGGCCCTCCCAACTCCAGTGGCACAGATGACGACTTGCAGTGACCACCCCT  
GCAGGCATCCAAAGGAGCACACATGCCATCGAGGAAGCCACCACAGAATCAGCAAATGGAATTCA  
GTAAGCTGTTCAAATTTCCAACTAAGCTGCCCGAATTGGTGATAATGTGAATCTTATC  
ATTGATTATATTATGGAATAGATTGAGACACATTGGATAGTCTAGAAAGAAATTAAATTCTTAATT  
TACCTGAAAATATTCTGAAATTTCAGAAAATATGTTCTATGTAGAGAAATCCAACTTTAAAAAA  
CAATAATTCAATGGATAAAATCTGTCTTGAATATAACATTATGCTGCCGGATGATATGCATAT  
TAAAACATATTGAAAAACTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM  
LTLPDILHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTPAGRLPTPSG  
TDDDFAVTTTPAGIQRSTHAIIEATTESANGIQ

**Signal peptide:**

amino acids 1-16

## **FIGURE 97**

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGCTCT  
CTTCTTGCTTGGCAAGCTGGACCAAGGGAGCCAGTCTTGGCTGCTTCGCCCCAGGCTCTCCCAAGGCCAGCCTGC  
GTCCCTGCCTGGCTGCTTGTGTCCTCGTCCCCAGGCTCTCCCAAGGCCAGCCTGC  
AGAGCTGTCTGTGAAGATTCCAGAAAATGGTGAATTTCCTTATACCTGACCAAGTGC  
CGCTGCCCGTGAGGGGCTGAAGGCCAGATCGTCTGTCAGGGACTCAGGCAAGGCAACTGAG  
GGCCCATTTGCTATGGATCCAGATTCTGGCTTCTGCTGGTACCCAGGCTGGACCGAGAGAGGA  
GCAGGCAGAGTACCAAGCTACAGTCACCCCTGGAGATGCAGGATGGACATGTCTTGTGGGTCAC  
AGCCTGTGCTTGTGACGTGAAGGATGAGAATGACCAAGGTGCCCCATTCTCTCAAGCCATCTAC  
AGAGCTGGCTGAGCCGGGTACCCAGGCCCTGGATCCCCCTCTCCTGAGGCTCAGACCG  
GGATGAGCCAGGCACAGCCAACCTGGATCTCAGATTCCACATCCTGAGCCAGGCTCCAGCCCAGC  
CTTCCCCAGACATGTTCCAGCTGGAGGCTCGGCTGGGCTCTGGCCCTCAGCCCCAAGGGGAGC  
ACCAGCCTGACCACGCCCTGGAGAGGACCTACCAGCTGGTACAGGTCAAGGACATGGGTGA  
CCAGGCCCTAGGCCACCAGGCCACTGCCACCGTGGAGCTCCATCATAGAGACACCTGGGTG  
CCCTAGAGCCTATCCACCTGGCAGAGAATCTCAAAGTCTATACCCGACACATGGCCAGGTA  
CACTGGAGTGGGGTGTATGTGCACTATCACCTGGAGAGCCATCCCCGGGACCCCTTGAAGTGA  
TGCAGAGGGAAACCTCTACGTGACCAGAGAGCTGGACAGAGAAGCCAGGCTGAGTACCTGCTCC  
AGGTGGGGCTCAGAATTCCATGGCGAGGACTATGCGGCCCCCTGGAGCTGACGTGCTGGT  
ATGGATGAGAATGACAACGTGCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCT  
CAGTCCACCAAGGTACTGAAGTGAATAGACTGTCAGCAGAGGATGCAGATGCCCGGCTCCCCA  
ATTCCCACGTTGTATCAGCTCTGAGCCCTGAGCCTGAGGATGGGTAGAGGGAGAGCCTC  
CAGGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGTCTCCACTCCAGCAGGCCAGAACAT  
CCTGCTCTGGTCTGGCCATGGACCTGGCAGGCCAGAGGGTGGCTCAGCAGCACGTGTAAG  
TCGAAGTCGAGTCACAGATATCAATGATCACGCCCTGACTCATCACTTCCAGAATTGGGCT  
ATAAGCCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCATGCTAACAGCCTATTGATGCTGA  
CCTCGAGCCCGCCTCCGCTCATGGATTGGCCATTGAGAGGGGAGACACAGAAGGGACTTTG  
GCCTGGATTGGGAGGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAAGAACCTCAGTTATGAG  
GCAGCTCCAAGTCATGAGGTGGTGGTGGTGGCAGAGTGTGGCAAGCTGGTGGGGCAGGCC  
AGGCCCTGGAGCCACCGCCACGGTGAATGTGCTAGTGGCCATGGCTCTTCTGCTGACCATC  
ACCAGGAGAGCTACGAGGCCAGTGTGCTAGGCTCAGGTTCTCCCTAGTCATGACTCAGAGGGCTGGCT  
CAGCCCTCCGACCCCATCAGCCGAACCCCTAGGTTCTCCCTAGTCATGACTCAGAGGGCTGGCT  
CTGCATGAGAATCTCGGGGAGGTGCAACCCGCCAGTCACCTTGCCCTGCAAGGGGCCAGCCTGGG  
ACACCTACACGGTGTGTTGGAGGCCAGGATACAGCCCTGACTCTTGCCCTGTGCCCTCCAA  
TACCTCTGCAACACCCGCCAGGATACAGCCCTGACTCTGCAAGGGGCCAGCAGGACCCGATCT  
GGCAGTGGCACGGTCCCTACAGCTTCACTGGTCCCAACCCACGGTCAACGGGATGGC  
GCCTCCAGACTCTCAATGGTCCATGCCCTACCTCACCTTGCCCTGCAATTGGGTGGAGGCCAGT  
GAACACATAATCCCCGTGGTGGCAGGCCACAATGCCAGATGTGGCAGCTGGTGGCTGAGTGAT  
CGTGTGCGCTGCAACGTGGAGGGCAGTGCATGCGCAAGGTGGGGCAGTAAGGGCATGCCA  
CGAAGCTGTCGGCAGTGGCATCTTGTAGGCACCCCTGGTAGCAATAGGAATCTCCTCATCTC  
ATTTTACCCACTGGACCATGTCAGGAAGAAGGCCGGATCAACCAGCAGCACAGCGTGCCCT  
GAAGGCCAGTGTCTGAATGGCCAGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAG  
TCCCTGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCCCTCA  
TCTGCCCTGGGTGGAGGCACCATCACCACCACTGGCAGAGCCTGGACACCAACTT  
TATGGACTGCCATGGAGTGTCCAATGTCAGGGTGTGCTTGGCCAATAATAAGCCCCAGAGAA  
CTGGGCTGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAG

## **FIGURE 98**

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSGKAT  
EGPFAMDPDSGFLLVTRALDREEQAQEYQLQVTLEMQDGHVLWGPQPVLVHKDENDQVPHFSQAI  
YRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRLGALALSPKG  
STSLDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSLPEIHLAENLKVLYPHMAQ  
VHWSGGDVHYHLESHPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQNSHGEDYAAPPLEHVL  
VMDENDNVPICPPRDPPTVSIPELSPPGTEVTRLSAEDADAPGSPNSHVYQLLSPPEPEDGVEGRA  
FQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGEGGSSTCEVEVAVTDINDHAPEFITSQIG  
PISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTEGTFGLDWEPDSGHVRLRLCKNLSY  
EAAPSHEVVVVVQSVAKLVGPGPGATATVTLVERVMPPKLDQESYEASVPISAPAGSFLLT  
IQPSDPISRTLRFSLVNDSEGWLICIEKFSGEVHTAQSLQGAQPGDTYTVLVEAQDTALTTLAPVPS  
QYLCTPRQDHGLIVSGPSKDPDLASGHGPYSFTLGPNPTVQRDWRQLTLNGSHAYLTTLALHWEV  
REHIIPVVVSHNAQMWMQLLVRVIVCRCNVEGQCMRKVGRMKGMPTKLSAVGILVGTIVAI  
LIFTHWTMSRKKDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

## **FIGURE 99**

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGTGCCCACGCCCTG  
AGTCCAAGATTCTCCCAGGAACACAAACCTAGGAGACCCACGCTCTGGAAGCACCAGCCTTTA  
TCTCTCACCTCAAGTCCCCTTCTCAAGAATCCTCTGTTTGCCTCTAAAGTCTGGTAC  
ATCTAGGACCCAGGCATCTGCTTCCAGCCACAAAGAGACAGATGAAGATGCAGAAAGGAAATG  
TTCTCCTATGTTGGTCTACTATTGCAATTAGAAGCTGCAACAAATTCCATGAGACTAGCACC  
TCTGCCAACACTGAGTCCAGTGTGATCTCCAGTGGAGCCACAGGCCACCAACTCTGGGTCCAG  
TGTGACCTCCAGTGGGTCAAGCACAGCCACCATCTCAGGGTCCAGGTGACCTCCAATGGGTCA  
GCATAGTCACCAACTCTGAGTCCATACAACCTCCAGTGGGTCAAGCACAGGCCACCAACTCTGAG  
TTCAGCACAGCCTCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACACCTCCAGTGG  
GGCCAGCACGCCACCAACTCTGAGTCCAGCACCCCTCCAGTGGGCCAGCACAGTCACCAACT  
CTGGGTCCAGTGTGACCTCCAGTGGAGCCAGCACTGCCACCAAACCTCTGAGTCCAGCACAGTC  
AGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAGCACACTCTCCAGTGGGCCAGCACAGCCAC  
CAACTCTGACTCCAGCACACCCCTCCAGTGGGCTAGCACAGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGCCAGCACGCCACCAACTCTGAGTCCAGCACAGTCAGTCCAGTAGGGCCAGCACT  
GCCACCAACTCTGAGTCCAGCACACCCCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCCAG  
AACGACCTCCAATGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACAGCCACCTCCAGTGGGCCA  
GCACAGCCACCAACTCTGACTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAG  
TCCAGCACGACCTCCAGTGGGCCAGCACGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG  
GGCTAGCACGCCACCAACTCTGACTCCAGCACACCCCTCCAGTGGGCCAGCACAGCCACCAACT  
CTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCC  
AGTGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGGGCCAACACAGCCAC  
CAACTCTGAGTCCAGCACAGTGTCCAGTGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACAA  
CCTCCAGTGGGCCAGCACGCCACCAACTCTGAGTCCAGCACACCCCTCCAGTGGGCCAGCAC  
GCCACCAACTCTGACTCCAGCACACCCCTCCAGTGGGCCAGCACAGCCACCAACTCTGAGTCTAG  
CACAGTGTCCAGTGGGATCAGCACAGTCACCAATTCTGAGTCCAGCACACCCCTCCAGTGGGCCA  
ACACAGCCACCAACTCTGGGCTCCAGTGTGACCTCTGAGGCTCTGGAAACAGCAGCTCTGACTTGA  
ATGCACACAACCTTCCATAGTGCATCTACTGCAGTGAGTGAGGCAAAGCCTGGTGGTCCCTGGT  
GCCGTGGAAATCTCCTCATACCCCTGGTCTCGGTTGCGGCCGTGGCTTGTGGCT  
TCTTCTCTGTGAGAAACAGCCTGCTGGTCAAGGAAACACCTTAAACAGCTGTCTACCCCT  
CATGGCCTCAACCATGGCCTGGTCCAGGCCCTGGAGGGAAATCATGGAGCCCCACAGGCCAG  
GTGGAGTCCTAAGTGGTCTGGAGGAGACCACTGATCATGCAGTGAGGAAAGAGACCTGGCA  
ACAGCGGGCCCTGAGCAGCCCGGAAGCAAGTGCCTGAGGAAAGAGACCTGGCA  
CCCAAGACCTGGTTCTCTCATCCAGGCCCTGGTCCAGGCCCTGGAGGGAAATCATGGAGGAGACCTGGCA  
AAATCTGAAAGAAGGTATTCTCACCTTCTTGCTTACAGACACTGGAAAGAGAAATACTATAT  
TGCTCATTAGCTAAGAAATAATACATCTCATCTAACACACAGACAAAGAGAAGCTGTGCTTG  
CCCCGGGGTGGGTATCTAGCTGAGATGAACCTAGTTAGGAGAAACCTCCATGCTGGACTC  
CATCTGGCATTCAAATCTCACAGTAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 100**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATISGS  
SVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESSTPSS  
GASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTSSGASTA  
TNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGAGTATNSES  
STTSSGASTATNDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTATNDSSTTSS  
GAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNSESSTVSSGASTA  
TNSESSTTSSGVSTATNSESSTTSSGASTATNDSSTSSEASTATNSESSTVSSGISTVTNSES  
STTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGSLVPWEIFLITLVSVVA  
AVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAPHRPRWSPNWFWRPVPSSI  
AMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

## **FIGURE 101**

GGCCGGACGCCCTCCCGTTACGGGATGAATTAAACGGCGGTTCCGCACGGAGGTGTGACCCCTA  
CGGAGCCCCAGCTGCCACGCACCCACTCGCGTCGCGCGTGCCTGCTGTACAGGTG  
GGAGGCTGGAACTATCAGGCTGAAAAACAGAGTGGTACTCTCTGGAAAGCTGGCAACAAAT  
GGATGATGTGATAATGCATTCCAGGGGAAGGGAAATTGTGGTGCTCTGAACCCATGGTCAATT  
AACGAGGCAGTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAGCTTGGAAATCAT  
GGTGTCAGGAAAGGGATTTACTTTACTGACTCTGTTGGGAAGCTTTGGAAAGCATT  
TCATGCTGAGTCCCTTTTACCTTGATGTTGAAACCCATCTGGTATCGCTGGATCAACAAAC  
CGCCTTGTGGCAACATGGCTACCCCTACCTGTGGCATTATTGGAGACCATGTTGGTGTAAAGT  
GATTATAACTGGGATGCATTGTCCTGGAGAAAGAAGTGTCAATTATCATGAACCATCGGACAA  
GAATGGACTGGATGTTCTGTGGAATTGCGTGCATAGCTACCTCAGATTGGAGAAAATT  
TGCCTCAAAGCGAGTCTCAAAGGTGTTGGATTGGTGGCCATGCAGGCTGCTGCCTATAT  
CTTCATTCAAGGAAATGGAAGGATGACAAGAGCCATTGAAAGACATGATTGATTACTTTGTG  
ATATTCACGAACCACTCAACTCCTCATATCCCAGAAGGGACTGATCTCACAGAAAACAGCAAG  
TCTCGAAGTAATGCATTGCTGAAAAAAATGGACTTCAGAAATATGAATATGTTTACATCCAAG  
AACTACAGGCTTACTTGTGGTAGACCGTCAAGAGAAGGTAAGAACCTTGATGCTGTCCATG  
ATATCACTGTGGCTATCCTCACAAACATTCCCTCAATCAGAGAAGCACCTCCTCCAAGGAGACTT  
CCCAGGGAAATCCACTTCACGTCCACCGGTATCCAATAGACACCCCTCCCCACATCCAAGGAGGA  
CCTTCAACTCTGGTGCCACAAACGGTGGGAAGAGAAGAAGAGGCTGCGTCCCTATCAAG  
GGGAGAAGAATTTATTACCGGACAGAGTGTCAATTCCACCTGCAAGTCTGAACTCAGGTC  
CTTGTGGTCAAATTGCTCTATACTGTATTGGACCCGTTCAGCCCTGCAATGTGCCTACTCAT  
ATATTGTACGACTCTGTTAAGTGGTATTATAATCACCATTGTAATCTTGCTGCAAGAGA  
GAATATTGGTGGACTGGAGATCATAGAACATTGCAATTGACTTTACACAAACAGCCACAT  
TTAAATTCAAAGAAAATGAGTAAGATTATAAGGTTGCCATGTGAAACCTAGAGCATATTTG  
GAAATGTTCTAAACCTTCAAGCTCAGATGCATTGCAATTGACTATGCGAATATTCTTACT  
GCCATCATTATTGTTAAAGATATTGCACTTAATTGCTGGGAAAATATTGCTACAATT  
TTAATCTCTGAATGTAATTGATACTGTCAGCAGGGAGTGATGGGGTGAATAACTT  
GGGCCAGAATATTAAACAATATCATCAGGCTTTAAA

## **FIGURE 102**

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFGIMVSWKGIYFILTLFWGSFFGSIFMLSP  
FLPLMFVNPSWYRWINNRLVATWLTPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTRMDWM  
FLWNCLMRYSYLRLEKICLKASLGPGFWAMQAAAYIFIHRKWKDDKSHFEDMIDYFCDIHEP  
LQLLIFPEGTDLTENSRSNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLDAVHDITVA  
YPHNIPQSEKHLLQGDFPREIHFHVRYPIDTLPTSKEDLQLWCHKRWEEKERLRSFYQGEKNF  
YFTGQSIPPCKSELRVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITIVIFVLQERIFGG  
LEIIELACYRLLHKQPHLNSKKNE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Transmembrane domains:**

amino acids 44-63, 90-108, 354-377

## **FIGURE 103**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCCACGGCTCTGCGCCTGAGACAGCTGGCTGACC  
TCCAAATCATCCATCCACCCCTGCTGTCATCTGTTCTAGTGTGAGATCAACCCACAGGAATA  
TCCATGGCTTTGTCATTTGGTTCTCAGTTCTACGAGCTGGTGCAGGACAGTGGCAAGT  
CACTGGACCGGGCAAGTTGTCAGGGCTTGGTGGGGAGGACGCCGTGTTCTGCTCCCTCT  
TTCCGTGAGACAGTGCAGAGGCTATGGAAGTGCAGGTTCTCAGGAATCAGTCCATGCTGTGTC  
CACCTCTACAGAGATGGGAAGACTGGGAATCTAACGAGATGCCACAGTATCGAGGGAGAACTGA  
GTTTGTGAAGGACTCCATTGCAAGGGGGCGTGTCTCTAAGGCTAAAAAACATCACTCCCTCGG  
ACATCGCCTGTATGGGTGCTGTTCAAGTCCCAGATTACGATGAGGAGGCCACCTGGGAGCTG  
CGGGTGCAGCACTGGGCTCACTTCTCTCATTTCCATGTTGGGATATGTTGACGGAGGTATCCA  
GTTACTCTGCTGTCTCAGGCTGGTCCCCAGGCCACAGCCAAGTGGAAAGGTCCACAAGGAC  
AGGATTGTCAGACTCCAGAGCAAATGCAGATGGGTACAGCCTGTATGATGTTGGAGATCTCC  
ATTATAGTCCAGGAAAATGCTGGGAGCATATTGTTCCATCCACCTTGCTGAGCAGAGTCATGA  
GGTGAATCCAAGGTATTGATAGGAGAGACGTTTCCAGCCCTCACCTGGCCTGGCTTCTA  
TTTACTCGGGTTACTCTGTTGCCCCGTGTTGATGGGATGATAATTGTTCTTC  
AAATCCAAAGGAAAATCCAGGGAACTGGACTGGAGAAGAAAAGCACGGACAGGCAGAATTGAG  
AGACGCCCGGAAACACGCACTGGAGGTGACTCTGGATCCAGAGACGGCTACCCGAAGCTCTGCG  
TTTCTGATCTGAAAATCTAACCATAGAAAGCTCCCCAGGAGGTGCTCACTCTGAGAAGAGA  
TTTACAAGGAAGAGTGTGGTGGCTCTCAGGGTTCCAGCAGGGAGACATTACTGGGAGGTGGA  
CGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGGATGACGTAGACAGGGGAAACA  
ATGTGACTTGTCTCCAAACAATGGGTATTGGTCTCAGACTGACAACAGAACATTGTT  
ACATTCAATCCCCATTATCAGCCTCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCT  
GGACTATGAGGGTGGGACCATCTCCTCTCAATACAATGACCAGTCCCTTATTATACCTG  
TGACATGTCAGTTGAAGGCTTGTGAGACCTATATCCAGCATGCTATGACGGAGAAAAG  
GGGACTCCCATATTCAATGTCAGTGTCTGGGAT**TGAG**ACAGAGAACAGCCCTGTTAAAGGGC  
CCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGTCTCCAGGCTGGCCAGCTTCT  
CCGGAGCCTGCGCACAGAGAGTCACGCCCTACTCTCTTAGGGAGCTGAGGTTCTGCCC  
TGAGCCTGCAAGCAGCAGTCACAGCTTCCAGATGAGGGGGAGTGGCTGACCCCTGTGGGAG  
TCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTAGTTGTGAAAA  
CTCCATCCAGCTAACGATCTTGAACAAGTCACAACCTCCAGGCTCTCATTTGCTAGTCACGG  
ACAGTGATTCTGCTCACAGGTGAAGGATAAAGAGAACAGAACATGTGAATCATGCTTGCAGGTT  
TGAGGGCACAGTGTGCTAATGATGTTTATATTACATTTCCACCATAAACTCTGTT  
TGCTTATTCCACATTAATTACTTTCTCTATACAAACATGCCATGGAATAGTTATTGAAACACC  
TGCTTGTGAGGCTAAAGAATAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAGCAT  
TACCTGATACAAAACAGGCAAAGAAAACAGAAGAAGGAAAACACAGGTCCATATCC  
CTCATTAAACAGACACAAAAATTCTAAATAAAATTGAACTAAACTAAACAATATATTAA  
AAGATGATATATAACTACTCAGTGTGGTTGTCACAAATGCAAGAGTTGGTTAATATTAAAT  
ATCAACCAGTGTAAATTCAAGCACATTAATAAGTAAAAAGAAAACCATAAAAAAAA

## **FIGURE 104**

MAFVLILVLSFYELVSGQWQVTGPGKVFQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAVVH  
LYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWELR  
VAALGSLPLISIVGYVDGGIQLLCLSSGWFQPTAKWKGPGQDLSRANADGYSLYDVEISI  
IVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCALCGVVMGMIIVFFK  
SKGKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAPQEVPHSEKRF  
TRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYWVRLLTTEHYFT  
FNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQHAMYDEEKG  
TPIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

## **FIGURE 105**

CCTTCACAGGACTCTCATTGCTGGTGGCAATGATGTATCGGCCAGATGTGGTAGGGCTAGGAAAAGAG  
TTTGGTGGAACCCCTGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTCCTGGCAGTGTGCATTGGA  
CTCACTGTTCATTATGTGAGATATAATCAAAGAACCTACAATTACTATAGCACATTGTCATTACAC  
TGACAAACTATATGCTGAGTTGGCAGAGAGGCTCTAACAAATTACAGAAATGAGCCAGAGACTTGAAT  
CAATGGTGGAAAATGCATTTATAATCTCCATTAAGGAAAGAATTGTCAAGTCTCAGGTTATCAAGTTC  
AGTCACACAGAACATGGAGTGTGGCTCATATGCTGTTGATTGAGATTTCACTCTACTGAGGATCCTGA  
AACTGTAGATAAAATTGTTCAACTTGTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAG  
ATCCTCACTCAGTAAAATTAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCATTGCTGCCGA  
ACACGAAGAAGTAAAACCTCTAGGTAGCTCAGAGTCAGGATCGTGGTGGACAGAAAGTAGAAGAGGGTGAATG  
GCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTTAATTATGCCACATGGC  
TTGTGAGTGTGCTCACTGTTACAACATATAAGAACCCCTGCCAGATGGACTGCTTCCTTGGAGTAACA  
ATAAAACCTTCGAAAATGAAACGGGTCTCCGGAGAAATAATTGTCCATGAAAATACAAACACCCATCACA  
TGACTATGATATTCCTTGAGAGCTTCTAGCCCTGTTACACAAATGCACTAGATAGAGTTGTC  
TCCCTGATGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAAT  
GATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACC  
TCAAGCTTACAATGACGCCATAACTCCTAGAAATGTTATGTGCTGGCTCCTAGAAGGAAAACAGATGCAT  
GCCAGGGTGAICTGGAGGACCACTGGTTAGTCAGATGCTAGAGATATCTGGTACCTGCTGGAATAGTG  
AGCTGGGGAGATGAATGTGCGAACCAACAGCCTGGTTTATAGAGTTACGGCCTGGCGGGACTG  
GATTACTTCAAAAACGGTATCTAAAGAGACAAAAGCCTCATGGAACAGATAACATTTTTTGTTGTTTG  
GGTGTGGAGGCCATTAGAGATACAGAAATTGAGACTGCAAACAGCTAGATTGACTGATCTCA  
ATAAAACTGTTGCTGATGCATGTATTTCTCCAGCTGTTCCGCACGTAAGCATCCTGCTTCTGCCA  
GATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATAACAAATTAC  
ATTACAGCCTGTATTCAATTGTTCTAGAAGTTGTCAGAAATTGACTTGTGACATAATTGTAAAT  
GCATATATAACAAATTGAAGCACTCCTTTCTCAGTCTCAGCTCAGTCTCTCATTTCAAGCAAATATCCATT  
TCAAGGTGAGAACAAAGGAGTGAAGAAAATAAGAAGAAAAAAACCCCTACATTATTGGCACAGAA  
AACTATTAGGTGTTCTTAGGAAATTAGAAATGATCATATTCAATTGAAAGCTCAAGCAAAGACA  
GCAGAACATCAACTCATATTAGGAAGTATGGAACTAAGTGAAGGAAGTCCAGAAAGAAGCCAAG  
ATATATCCTATTTCATTTCAACAAACTACTATGATAATGTGAAGAAGATTGTTGTTGTGACCT  
ATAATAATTATACAAACTTCATGCAATGTAATTGTTCTAAGCAAATTAAAGCAAATTATTAAACATTG  
TTACTGAGGATGTCAACATATAACAATAAAATATAACACCA

## **FIGURE 106**

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDKLY  
AEFGREASNNFTEMSRMVKNAFYKSPLREFVKSQVIKFQQKGVLAHMLLICRFHSTED  
PETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQSLRIVGG  
TEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIKPSKMKRGL  
RRIIVHEKYKHPHSDYDISLAELSSPVYTNAVHRVCLPDASYEFQPGDVMFVTGFGALKNDGYS  
QNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGDGGPLVSSDARDIYLAG  
IVSWGDECAPNPKPGVYTRVTALRDWITSKTGI

**Transmembrane domain:**

amino acids 21-40 (type II)

## **FIGURE 107**

AGAGAAAAAGCGCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCGCGAAGAAGTTCCCTG  
CCCCGATGAGCCCCCGCGTCCGCTCCCGACTATCCCAGCGGGCGTGGGGCACCGGGCCAGC  
GCCGACGATCGCTGCCGTTTGCCTTGGAGTAGGATGTGGTGAAGGATGGGGCTTCTCCCTT  
ACGGGGCTCACAATGGCCAGAGAAAGATTCCGTGAAGTGTCTGCGCTGCCTACGCCCTCAA  
TCTGCTCTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTGGATGAGGGACTACCTAA  
ATAATGTTCTCACTTTAACAGCAGAAACGAGGGTAGAGGAAGCAGTCATTGACTTACCTTCC  
GTGGTTCATCCGGTCTGATTGCTGTTGCTTCTTATCATTGTTGGGATGTTAGGATATTG  
TGGAAACGGTGAAGAAGAAATCTGTTGCTTCTGCTGGTACTTTGGAAAGTTGCTGTCAATTCT  
GTGAGAACTGGCTGTGGCCTTGGACATATGAACAGGAACCTATGGTCCAGTACAATGGTCA  
GATATGGTCACTTGAAGGCCAGGATGACAAATTATGGATTACCTAGATATCGGGGCTTACTCA  
TGCTTGAATTTCAGAGAGGTTAACGTGTGGAGTATATTCACTGACTGGTGG  
AAATGACAGAGATGGACTGGCCCCAGATTCCTGCTGTAGAATTCCAGGATGTTCCAAA  
CAGGCCACCAGGAAGATCCTAGTGAACCTTATCAAGAGGGTTGGGAAGAAAATGATTCTT  
TTTGAGAGGAACCAAACAACGTGAGGTGCTGGGATCTCCATTGGGTGACACAAA  
TCCTGGCCATGATTCTACCAATTACTCTGCTCTGGGCTCTGATTATGATAGAAGGGAGCCTGG  
ACAGACCAAATGATGTCCTTGAAGAATGACAACCTCAGCACCTGCTATGTCCTCAGTAGAACT  
GTTGAAACCAAGCCTGTCAAGAATCTTGAACACACATCCATGGCAACAGCTTAATACACACT  
TTGAGATGGAGGAGTTAAAAAGAAATGTCACAGAAGAAAACCACAAACTTGTATTGGACT  
TGTGAATTGGAGTACATACTATGTGTTTCAAGAAATATGTAGAAATAAAATGTTGCCATAAAA  
TAACACCTAACGATATACTATTCTATGCTTAAAATGAGGATGAAAGTTTCATGTCATAAGTC  
ACCACCTGGACAATAATTGATGCCCTAAAATGCTGAAGACAGATGTCATACCCACTGTTGACCC  
TGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTCGCA  
TCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGTTGATTACTTCAACAA  
CTAGTATATAAAAGTACTAATTAAATGCTAACATAGGAAGTTGAAAAACTAAACTTATTATA  
CTCAGCGATCTATTCTCTGATGCTAAATAATTATATCAGAAAACCTTCAATATTGGTACT  
ACCTAAATGTGATTGGTACTTAAATCTTACCACTTAAAGAGCAAGCTAACACAT  
TGTCTTAAGCTGATCAGGGATTGGTATATAAGCTGTGTTAAATCTGTATAATTCACTGCGAT  
TTCAGTTCTGATAATGTTAAGAATAACCAATTGAAAAGGAAATTGTCCTGTATAGCATCATT  
ATTGGTATTGGCTTCTGTTAATAAGCTTACTATTCTGCTGGCTTATATTACACATATAAC  
TGTTATTAAATACCTAACCAACTTAAATTGAAAATTACCACTGTCATAGGAATCATTATTC  
AGAATGTAGTCTGGCTTTAGGAAGTTAAATAAGAAAATTGACACATAACTTAGTTGATTCAA  
AAGGACTTGTATGCTGTTTCTCCAAAGAAGACTCTTGTGACACTAAACACTTTAAAAAA  
GCTTATCTTGCCTCTCCAAACAAGAAGCAATAGTCTCCAAGTCATATAAAATTCTACAGAAAA  
TAGTGTCTTTCTCCAGAAAATGCTGTGAGAATCATTAAACATGTGACAATTAGAGATT  
CTTGTGTTATTCACTGATTATAACTGTGGCAAATTACACAGATTATTAATTTTACAA  
GAGTATAGTATATTATTGAAATGGAAAAGTCATTTACTGTATTGTGATTGTTAT  
TTCTCAGAATATGAAAGAAAATTAAATGTGTCATAAAATATTCTAGAGAGTAA

## **FIGURE 108**

MAREDSVKCLRCLLYALNLLFWIIMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHP  
VMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVT  
LKARMNTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQ  
EDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLSIGVTQILAMILTITLLWALYYDRREPGTDQM  
MSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

## **FIGURE 109**

CCAAGGCCAGAGCTGTGGACACCTTATCCCCTCATCCTCATCCTCTTCCCTGTATAAGCCCCTACCAAGTGCT  
GATAAAGTCTTCTCGTAGAGCCTAGAGGCCCTAAAAAAAGTGCCTGAAAGAGAAGGGACAAAGGAACA  
CCAGTATTAAAGAGGATTTCCAGTGTTCAGTGGCAGTTGGTCCAGAAGGATGCCTCCATTCCTCTCACCTG  
CCTCTCATCACAGGCACCTCCGTGTCAACCGTGGCCCTAGATCCTGTCTGCTTACATCAGCCTGAATGAGC  
CCTGGAGGAACACTGACCACCAAGTGGATGAGTCAGGTCTCTATGTGACAACCATGTGAATGGGAG  
TGGTACCACTTCACGGCATGGCGGAGATGCCATGCCTACCTCTGCATACAGAAAACCACTGTGGAACCCA  
CGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCAGGGCATTGTGCAACGCCAGGTTGTGCCAGCT  
TCAATGGAACACTGCTGTCTGGAACACACAGGGAGAAGTCAAGGCTTGCCCTGGAGGCTACTATGTGTATCGT  
CTGACCAAGCCCAGCGCTGCTTCCACGTCTACTGTGGTCATTGACATCTGCGACGAGGACTGCCATGG  
CAGCTGCTCAGATACCAGCGAGTGCACATGCGCTCCAGGAACGTGCTAGGCCCTGACAGGAGACATGCTTG  
ATGAAAATGAATGTGAGCAAACACAGGTGGCTGCACTGAGATCTGTGTGAACCTCAAAACTCCTACCGCTGT  
GAGTGTGGGTTGGCCGTGTGCTAAGAAGTGTGCAAGACTTGTGAAGACGTTGAAGGATGCCACAATAACAA  
TGGTGGCTGCAGCCACTTGTGCTTGGATCTGAGAAAAGGCTACCAAGTGTGAATGTCCCCGGGCCTGGTGT  
CTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAATCAAATGCCATTGAAGTGAACATCCCCAGGGAG  
CTGTTGGTGGCCTGGAGCTTCTGACCAACACCTCTGCCAGGGAGTGTCAACGGCACCCATGTCAACAT  
CCTCTCTCTCAAGACATGTGGTACAGTGGTCATGTGGTGAATGACAAGATTGTGCCAGCAACCTCGTGA  
CAGGTCTACCCAAGCAGACCCCCGGGAGCAGCAGGGACTCATCATCGAACAGCAAGCTGCTGATCCCCGTG  
ACCTGCGAGTTCCACGCCGTACACCATTCTGAAGGATACGTTCCAACCTTCGAAACTCCCCACTGGAAT  
CATGAGCCGAAATCATGGGATCTTCCCACTCTGGAGATCTTCAAGGACAATGAGTTGAAGAGCCTTAC  
GGGAAGCTCTGCCACCCCAAGCTCGTGAACCTCTACTTGGCATTGAGCCGTGGTGCACGTGAGCGGC  
TTGGAAGCTTGGTGGAGAGCTGCTTGCACCCACCTCCAGATCAGCAGGACTCTGAAATACTACCTCAT  
CCGGGATGGCTGTTCAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTGTCTGGAGTG  
TCCCTGCTTCAAGTTGTGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGTTCTGTCTGGAGTG  
TTGGACGAGCGTCTCCGCTGTCCCCAGGGTGTGCCACCCGGAATGGCTGTGGGCAGGAGGAGAGGACTCAGC  
CGGTCTACAGGGCCAGCCTAACAGGCGGCCGATCCGCATCAGTGGAGGACTAGTTCGTAGCCATACCTC  
GAGTCCCTGCATTGGACGGCTCTGCTCTTGGAGCTCTCCCCCACCGCCCTCTAAGAACATCTGCCAACAGC  
TGGGTTAGACTTCACACTGTGAGTCAGACTCCAGCACCACACTCTGATTCTGGTCAATTCAAGTGGCA  
CAGGTACAGCACTGCTGAACAATGTGGCCTGGTGGGTTCATCTTCTAGGGTTGAAAACACTAAACTGTCCA  
CCCAGAAAGACACTCACCCATTCCCTCATTTCCACTACCTAAACACTGTGTATGGTGAATCAGAC  
CACAAAATCAGAAGCTGGGTATAATATTCAAGTACAAACCTAGAAAAATTAACAGTTACTGAAATTATGA  
CTTAAATACCAATGACTCCTAAATATGTAATAGTTACCTTGAAATTCAATTCAAATGCAGACTAA  
TTATAGGAATTGGAAGTGTATCAATAACAGTATATAATT

## **FIGURE 110**

MPPFLLLTCLFITGTSVSPVALDPCSAIISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFTGMAGDAMP  
TFCIPEHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCLWNTTVEVKACPGGYYVYRLTKPSVCFHV  
YCGHFYDICDEDCHGSCDTSECTCAPGTVLGPDRCQTCFDENECEQNNGGCSEICVNLKNSYRCECGVGRV  
LRSRGKTCEDVEGCHNNNGGCSHCLGSEKGYQCECPRLVLSEDNHTCQVPVLCKSNAIEVNIPRELVGG  
LELFLLNTSCRGVSNGTHVNILFSLKTCGTVVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVT  
CEFPRPLYTISEGYVPNLRNSPLEIMSRNHGIFPFTLEIFKDNEFEEPYREALPTLKLRSLSYFGIEPVVHV  
SGLESLVESCATPTSKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRV  
LVCGVLDERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

**Tyrosine kinase phosphorylation sites.**

amino acids 411-418, 443-451

**N-myristoylation sites.**

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,  
522-528, 531-537

**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

**ZP domain proteins.**

amino acids 431-457

**Calcium-binding EGF-like proteins.**

amino acids 191-212, 232-253

## **FIGURE 111**

GAGAGAGGCAGCAGCTGCTCAGGGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCCCTGCACACTCGG  
GCCTCCTCCAGCCAGTGCCTGACCAGGGACTCTGACCTGCTGCCAGCCAGGACTGTGTGGGAGGCCT  
CCTGCTGCCTGGGGTGAACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGCATGT  
TACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTC~~AAACCC~~CTGCGAAACCCGTATCCCC  
ATGGAGACCTTCAGAAAGTGGGATCCCCATCATCATAGCACTACTGAGCCTGGAGTATCATCATIGT  
GGTTGTCTCATCAAGGTATTCTGGATAAAACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGA  
GGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCAGTGTCAAGAGCTTC  
CCCGAAGGGCCTGCAGTGGCAGTCGCCTCTCAAGGACCGATCCACACTGCAAGGTGCTGGACTCGGCCAC  
AGGGAACTGGTTCTCTGCCTGTTGACAACACTTCACAGAAGCTCGCTGAGACAGCCTGTAGGCAGATGG  
GCTACAGCAGAGCTGTGGAGATTGCCAGACCAAGGATCTGGATGTTGAAATCACAGAAAACAGCCAG  
GAGCTTCGCATGCGGAACCTCAAGTGGCCCTGTCAGGCTCAGGCTCTGGTCTCCCTGCACTGCTTGCCTG  
TGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGGAGGAGGCTCTGTGGATTCTGGCCTTGGCAGG  
TCAGCATCCAGTACGACAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGCCTCACGGCA  
GCCCACTGCTTCAGGAAACATACCGATGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGCAG  
CTTCCCATCCCTGGCTGTGGCAAGATCATCATCATTGAATTCAACCCATGTACCCAAAGACAATGACA  
TCGCCCTCATGAAGCTGCAGTCCACTCACTTCTCAGGCACAGTCAGGCCATCTGTCTGCCCTTCTT  
GATGAGGAGCTCACTCCAGGCCACCCACTCTGGATGTTACGAAGCAGAATGGAGGGAA  
GATGTCTGACATACTGCTGCAGGGCTCAGTCCAGGTCTTGACAGCACACGGTGCAATGCAAGCAGTGC  
ACCAGGGGAAGTCACCGAGAAGATGATGTGCAGGCATCCCGGAAGGGGTGTGGACACCTGCCAGGGT  
GACAGTGGTGGCCCTGATGTAACCAATCTGACCAAGTGCAGGCCATGTTAGCTGGGCTATGG  
CTGGGGGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCT  
GGAAGGCTGAGCTGTAATGCTGCTGCCCTTGCAGTGCAGGGCCTCCCTGCCCTGCCACCT  
GGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCTGGTACACCCCTCTGCCACAGCCTCAGCAT  
TTCTGGAGCAGCAAAGGCCCTCAATTCCGTAAAGAGACCCCTCGCAGGCCAGGGCGCCAGAGGAAGTCA  
GCAGCCCTAGCTGCCACACTTGGTGCCTCAGCATCCCAGGGAGAGACACAGCCACTGAACAAGGTCT  
CAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCACACTGAAATGGAAGCAGGCTGTCTGTAAAAGCC  
CAGATCACTGTGGCTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGCGCTTCAACCATCCCCAA  
GCCTACTAGAGCAAGAAACCAAGTGTAAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTTACCT  
ACTGTTGTCATTGTTATTACAGCTATGCCACTATTAAAGAGCTGTAAACATCTGGAAAAAAA  
AAAA

## **FIGURE 112**

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYYFLCG  
QPLHFIPRKQLCDGEELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSACFDN  
FTEALAEETACRQMGYSRAVEIGPDQDLDVVEITENSQELRMRNSSGPCLSGSLVSLHCLACGKSL  
KTPRVVGGEEASVDSWPWQVSIQYDKQHVCAGGSILDPHWVLTAAHCFRKHTDVFNWKVRAGSDKL  
GSFPSLAVAKIIIIIEFPMPKNDNDIALMKLQFPLTFSGTVRPICLPPFDEELTPATPLWIIIGWG  
FTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTQCQGDGGPLMYQS  
DQWHVVGIVSWGYYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

### **FIGURE 113**

GGCTGGACTGGAACCTCTGGTCCAAGTGATCCACCCGCCTCAGCCTCCAAAGGTGCTGTGATTA  
TAGGTGTAAGCCACCGTGTCTGCCCTGAACAACCTTTCACTGCTGCTACTCCTACCTACATTAAATC  
TGAAC TGCTAGGATTCTGACTATGCTGTGGCTAGTGCTCCTACTCCTACCTACATTAAATC  
TGT TTTTGTCTCTGTAACTAGCCTTACCTCCTAACACAGAGGATCTGTCACTGTGGCTCT  
GGCCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCACACCGTCCCCTGAAG  
CCGGGGACAGCCTCACCTGCTGCCCTCTCGCTGGAGCAGTGCCCTACCAACTGTCTCACGTCT  
GGAGGCAGTGACTCGGGCAGTGAGGTAGCTGAGCCTCTGGTAGCTGCGGCTTCAAGGTGGC  
CTTGCCCTGGCGTAGAAGGGATTGACAAGCCGAAGATTCATAGGCATGGCTCCACTGCC  
AGGCATCAGCCTGCTGACTCACTGCCCTGGGCCAGGACGGCCGTGGACACCTGCTCA  
GAAGCAGTGGGTAGACATCACGCTGCCGCCATCTAACCTTTCATGTCCTGCACATCACCTG  
ATCCATGGGCTAATCTGAACTCTGCTCCAAGGAACCCAGAGCTTGAGTGAGCTGTGGCTCAGACC  
CAGAAGGGTCTGCTTAGACCACCTGGTTATGTGACAGGACTTGCAATTCTCTGGAACATGAGG  
GAACGCCGGAGGAAAGCAAAGTGGCAGGGAAAGGAACCTGTGCAAATTATGGTCAGAAAAGATG  
GAGGTGTTGGTTATCACAAGGCATCGAGTCTCTGCATTCACTGAGCTGACATGTGGGGAAGGGCTG  
CCGATGGCGCATGACACACTCGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGAT  
CCACGTACAGCTGCTGAAGGGCAACTGCAGGCCATGCTCTCATCAGCCAGGCAGCAGCCAAA  
TCTGCGATCACCAGCCAGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACATTCTCTCCC  
CTCCTCCCTCTGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGG  
GGCTAATGGCTCAGTGTGGCCAGGAGGTAGCAAGCAGGCTGAGAGCTGATCAGAAGGCCGTGCT  
GTGCGAACACGGAAATGCCCTCAGTAAGCACAGGCTGCAAATCCCAGGCAAAGGACTGTGTGG  
CTCAATTAAATCATGTTCTAGTAATTGGAGCTGCTTCAAGACCAAGGAGCTAGAGCTTGGTT  
CAAATGATCTCCAAGGGCCCTATACCCAGGAGACTTGATTTGAATTGAAACCCCAAATCCA  
AACCTAAGAACCAAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGTGGCTGTAATGCCAACAT  
TTTGGGAGGCGAGGCAGGTAGATCACCTGAGGTAGGCTCAGGAGTTCAAGACCAAGGCCGTGCAACATGG  
TGAAACCCCTGTCTACTAAAAATACAAAAAAACTAGCCAGGCAAGGTGTGGCTGCTGTATC  
CCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTGAAACCTGGGAGGTGAAGGAGGCTGAGACA  
GGAGAACATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAGAATTA  
TGGTTATTGTAA

## **FIGURE 114**

MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDSLWPKPDLHSGTRTEVSTHTVPSKPGTASPC  
WPLAGAVPSPTVSRLALTRAVQVAEPLGSCGFQGGPCPGRRD

**Signal peptide:**

amino acids 1-15

## **FIGURE 115**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGGCAA  
AGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTAAATCCAAGAAA  
ATATGTAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCTAATTGTCCT  
GTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTT  
TCTACAGCAATGGAGAGAAGAAGATTTACATGAAATTGATCCTGTGACCAGAACTGAAATA  
TTCAGAAGCGAAATGGCACTGATGAAACATTGAAAGTGCACGACTTTAAAACGGATACTGG  
CATCTACTCGTGGTCTCAAAAATGTTTATCAAAACCTCAGATTAAGTGATTCTGAATT  
CTGAACCAGAAGAGGAAATAGATGAGAATGAAAGAAATTACCAACTTCTTGAAACAGTCAGTG  
ATTGGGTCCCAGCAGAAAGCCTATTGAAAACCGAGATTTCTTAAATCCTGAAACAGTCAGTG  
GATTTGTGATAACGTGACCATGTATTGGATCAATCCCCTCTAATATCAGTTCTGAGTTACAAG  
ACTTTGAGGAGGGAGGAGAAGATCTTCACTTCCCTGCCAACGAAAAAAAGGGATTGAAACAAAT  
GAACAGTGGTGGTCCCTCAAGTGAAGTAGAGAAGACCCGTACGCCAGACAAGCAAGTGAGGA  
AGAACTCCAATAATGACTATACTGAAATGAAATGATCCCCTGCTGGATGAGAGAG  
GTTATTGTTGTATTACTGCCGTCAGGCAACCGCTATTGCCGCCGCTGTGAAACCTTACTA  
GGCTACTACCCATATCCACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCCTG  
TAACTGGTGGTGGCCCGCATGCTGGGAGGGCTTAATAGGAGGTTGAGCTCAAATGCTAAAC  
TGCTGGCAACATATAATAATGCTATTCAATGAAATTCTGCCATGAGGCATCTGGCCCT  
GGTAGGCCAGCTCTCCAGAATTACTGTAGGTAATTCTCTCTCATGTTCTAATAAACTTCTACA  
TTATCACCAAAAAAAAAAAAAAA

## **FIGURE 116**

MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTILFWGSKHFWPEVPKKAYDME  
HTFYNSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP  
EFSEPEEEIDENEITTTFEQSVIWVPAEKPIENRDFLKNSKILEICDNVTMYWINPTLISVSE  
LQDFEEEGEDLHFPAKEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENGIEFDPLD  
ERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWVARMLGRV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

## **FIGURE 117**

GAGCTCCCTCAGGAGCGCGTTAGCTCACACCTCGCAGCAGGAGGGCGGCAGCTCTCGCAGGCGCA  
GGCGGGCGGCCAGGATCATGTCCACCACCATGCCAAGTGGTGGCGTCCCTCTGTCCATCCTGGGGCT  
GGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGGACCTGTACGACAACCCCGTCACCT  
CCGTGTTCCAGTACGAAGGGCTCTGGAGGAGTCGAGGAGAGTTCAAGGCTTCAACGAATGCAGGCC  
TATTCACCATCCTGGACTTCCAGCCATGCTCAGGCAGTGGAGCCCTGATGATCGTAGGCATCGTCT  
GGGTGCCATTGGCCTCTGGTATCCATCTTGCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTG  
CCAAAGCCAACATGACACTGACCTCCGGATCATGTTCAATTGTCAGGTCTTGTCAGGCAATTGCTGGAGTG  
TCTGTGTTGCCAACATGCTGGTACTAATTCTGGATGTCCACAGCTAACATGTACACCGGATGGTGG  
GATGGTGCAGACTGTTCAAGACCAGGTACACATTGGTGCAGCTGGGGCTGGCAGGACTCAAGGCCAGCAGTGGCT  
TCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGCTGGCACCAGAAGAAACCAACTACAAA  
GCCGTTCTTATCATGCCCTCAGGCACAGTGTGCCTACAAGCCTGGAGGCTCAAGGCCAGCAGTGGCT  
TGGGTCCAACACCAAAAAACAAGAAGATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTATC  
CTTCCAAGCAGCACTATGTGTAATGCTCTAACAGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCA  
CCCCAAAACAAGGAGATCCCATCTAGATTCTCTTGACTCACAGCTGAAAGTTAGAAAAGCCT  
CGATTTCATCTTGGAGAGGCCAATGGTCTTAGCCTCAGTCTGTCTCAAATATTCCACCATAAAACA  
GCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCACATTCTCTATTCTTTAAATATAACT  
TTCTACTCTGATGAGAGAATGTGTTTAATCTCTCTCACATTCTGATGATTAGACAGACTCCCCCTC  
TTCCCTCTAGTCATAAAACCCATTGATGATCTATTCCAGCTTATCCCCAAGAAAATTGGAAAGGAAA  
GAGTAGACCAAAAGATGTTATTCTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAA  
ACACTTACTGAAGAAGAACAATAAGAGAAAGATATTGTAATCTCTCCAGGCCATGATCTGGTTCTTCTT  
ACACTGTGATCTAAAGTTACCAACCAAAAGTCATTTCAGTTGAGGCTCTGAGCTCTCCACTGGAGTCTTCTGT  
TTGACATCTCTTATTACAGCAACACCATTCTAGAGTTGAGCTCTGAGCTCTCCACTGGAGTCTTCTGT  
CGCGGGTCAGAAAATTGCTCTAGATGAATGAGAAAATTATTCTTAAATTAAAGCTAAATATAGTTAA  
AATAAAATAATGTTAGTAAATGATACTATCTCTGTAAATAGCTCACCCCTACATGTGGATAGAAG  
GAAATGAAAAATAATTGCTTTGACATTGTCTATGGTACTTTGTAAGTCATGCTTAAGTACAAATTCC  
ATGAAAAGCTCACACCTGTAATCTGACTTTGGAGGCTGAGGAGGAAGGACTACTGAGCCAGAAGT  
TCGAGACTAGCCTGGCAACATGGAGAAGCCCTGTCTCACAAATACAGAGAGAAAAATGCCAGTC  
TGGTGGCATACACCTGTAATCTGACTTTGGAGGCTGAGGAGGACTACTGAGCCAGGGAGGT  
TGGGGCTGCAGTGAGGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGCTAA  
AATAAAAATAATGAAACACAGCAAGTCCTAGGAAGTAGGTTAAAACATAATTCTTAA

## **FIGURE 118**

MSTTCQVVAFLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTECRP  
YFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFIVSGL  
CAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGVWAGGLTLIGGVMMCIA  
CRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQSYP SKHDY  
V

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

## **FIGURE 119**

GGAAAAACTGTTCTCTGTGGCACAGAGAACCTGCTCAAAGCAGAAGTAGCAGTCCGGAGTCC  
AGCTGGCTAAAACATCCCAGAGGATAATGCAACCCATGCCTAGAAATCGCTGGCTGTTCTTG  
GTGGTGTGGAATGGGGCACAGTGGCTGACTGTCATGCCTCAGTGGAGAGTGTGCGGCCTTCATT  
GAAAACAAACATCGTGGTTTGGAAACTCTGGAGGACTGTGGATGAATTGCGTGAGGCAGGCTAA  
CATCAGGATGCAGTGCAAAATCTATGATCCCTGCTGGCTTTCTCCGGACCTACAGGCAGCCAG  
GACTGATGTGCTGCTCCGTGATGTCCTTCTGGCTTCATGATGCCATCCTGGCATGAAATGC  
ACCAGGTGCACGGGGACAATGAGAAGGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCAT  
CATCACGGGCATGGTGTGCTATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTCTATA  
ACTCAATAGTGAATGTTGCCAAAAACGTGAGCTGGAGAAGCTCTACTTAGGATGGACCACGGCA  
CTGGTGCTGATTGTTGGAGGAGCTCTGTTCTGCGTTTGTGCAACGAAAGAGCAGTAGCTA  
CAGATACTCGATACTTCCCATCGCACAACCCAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCG  
TCTACTCCAGAAGTCAGTATGTGTAGTTGTATGTTTTAACTTACTATAAAGCCATGCAAATG  
ACAAAAATCTATATTACTTCTCAAAATGGACCCCAAAGAAACTTGTATGTTACTGTTCTTAACGCCT  
AATCTTAATTACAGGAACGTGCACTCAGCTATTATGATTCTATAAGCTATTCAGCAGAATGAGATA  
TTAAACCAATGCTTGATTGTTAGAAAGTATAGTAATTGTTCTAAGGTGGTCAAGCATTCTA  
CTCTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTACTACTGTAATTCTCC  
ACGACATAGCATTATGTACATAGATGAGTGTAAACATTATCTCACATAGAGACATGCTTATGGT  
TTTATTAAATGAAATGCCAGTCCATTACACTGAATAAAATAGAAACTCAACTATTGCTTCAGGGAA  
ATCATGGATAGGGTTGAAGAAGGTTACTATTAAATTGTTAAAAACAGCTTAGGGATTAATGCTCCA  
TTTATAATGAAGATTAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATAT  
GCTGTTTTAGCCTAGGAGTTAGAAATCCTAACTTCTTATCCTTCTCCAGAGGGCTTTTT  
CTTGTGTTAAATTAAACATTAAACGAGATATTGTCAAGGGCTTGCAATTCAAAGCTT  
TTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGATGGTTAGGAAAGT  
AAAATTTGTTGTATTGAAGAAGAATGATGCAATTGACAAGAAATCATATGTTGATGGAT  
ATATTAAATAAGTATTGAGTACAGACTTGAGGTTCATCAATATAAAAGAGCAGAAAAATA  
TGTCTGGTTTCAATTGCTTACCAAAAAACAAACAAAAAAAGTGTCTTGTGAGAAACTTCACCT  
GCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTGTTCTGTGAAAAATAATTCTTGT  
CCATTCTGTTAGTTACTAAAATGTAAACTGTATTGTTCTGTTATTCAAATTGAA  
ACTGACAATCCAATTGAAAGTTGTGTCGACGTCTGCTAGCTTAAATGAATGTGTTCTATTGCTT  
TATACATTATTAATAAAATTGTACATTCTAATT

## **FIGURE 120**

MATHALEIAGLFLGGVGMVGTAVTVMPQWRVSIFIENNIVVFENFWEGLWMNCVRQANIRMQCK  
IYDSLLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLAGIIFIITG  
MVVLIPVSWVANAIIRDYNSIVNVAQKRELGEALYLGWTALVLIVGGALFCCVFCCNEKSSY  
RYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

## **FIGURE 121**

GGAGAGAGGCGCGCGGGTGAAGGCGATTGATGCAGCCTGCGCGGCCTCGGAGCGCGCGAG  
CCAGACCGCTGACCACGTTCTCCTCGGTCTCCTCCGCTCCAGCTCCCGCTGCCAGCC  
GGGAGCCATGCGACCCCAGGGCCCCGCCGCCTCCCCGAGCGGCTCCGCGGCCCTGCTGCTCC  
TGCTGCTGCAGCTGCCCGCGCCGTGAGCGCCTCTGAGATCCCAAGGGGAAGCAAAGGCGAG  
CTCCGGCAGAGGGAGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAGCAGGAGTGCC  
TGGTCGAGACGGGAGCCCTGGGCCAATGTTATTCCGGTACACCTGGATCCCAGGTGGATG  
GATTCAAAGGAGAAAAGGGGGATGTCTGAGGGAAAGCTTGAGGAGTCTGGACACCCAACCTAC  
AAGCAGTGTTCATGGAGTTCATGAAATTATGGCATAGATCTTGGAAAATTGCGGAGTGTACATT  
TACAAAGATGCGTCAAATAGTGCTCTAAGAGTTGTCAGTGGCTCACTCGGCTAAATGCA  
GAAATGCATGCTGTCAGCGTTGGTATTCACATTCAATGGAGCTGAATGTTCAAGGACCTCTCCC  
ATTGAAGCTATAATTATTGGACCAAGGAAGCCCTGAAATGAATTCAACAATTAAATTATCATCG  
CACTTCTCTGTGGAAGGACTTGTGAAGGAATTGGTGGATTAGTGGATGTTGCTATCTGGG  
TTGGCACTTGTCAGATTACCCAAAAGGAGATGCTTCACTGGATGGAATTGAGTTCTCGCATC  
ATTATTGAAGAACTACCAAAATAAATGCTTAATTTCATTTGCTACCTCTTTTATTATGCC  
TTGGAATGGTTCACTTAAATGACATTAAATAAGTTATGTATACTCTGAATGAAAAGCAAAG  
CTAAATATGTTACAGACCAAGTGTGATTTCACACTGTTTAAATCTAGCATTATTCACTTGC  
CTTCAATCAAAAGTGGTTCAATATTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATT  
CTCTCAACCTATAATTGGAATATTGTTGGTCTTTGTTCTCTTAGTATAGCATTGTTA  
AAAAAAATAAAAAGCTACCAATCTTGTACAATTGTAAGAATTTTTTATATCTGT  
TAAATAAAAATTATTCCAACA

## **FIGURE 122**

MRPQGPAA SPQR LRG LLLL LQLP APSS ASEIPKGKQKAQLR QREVVDLYNGMCLQGPAGVPGR  
DGSPGANV IPGTPG I PGRDGF KGEK GECL RESFEE SWTPNYKQCSWSSLNYGIDL GKIA ECTFTK  
MRSNSALRVL FSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAI IYLDQGSPEMNSTINI HRTS  
SVEGLCEGIGAGLVDV A I WVGTCSDYPKG DASTGWNSVSRIII EELPK

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

## **FIGURE 123**

GCTGAGCGTGTGCGCGTACGGGCTCTCGCTTCTGGCTCCAACGCAGCTGTGGCTGAA  
CTGGGTGCTCATCAGGGAACTGCTGGGCTATGAAATACAGATGTGGCAGCTCAGGTAGCCCCAA  
ATTGCCTGGAAGAATACATCATGTTTCGATAAGAAGAAATTGAGGATCCAGTTTTTTTA  
ACCGCCCCCTCCCCACCCCCAAAAAAACTGTAAGAGATGCAAAACGTAATATCCATGAAGATCC  
TATTACCTAGGAAGATTGATTTGCTGCGAATGCGGTGTTGGATTATTGTTCTGGAG  
TGGTCTCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCAAGGGTCCAATT  
TCTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGACGCTGACAGGGCTGTCATGCAACTG  
GCCCTAAAGCCAAAGCAAAAGACCTAAGGACGACCTTGAACAATACAAGGATGGTTCAATG  
TAATTAGGCTACTGAGCGGATCAGCTGAGCACTGGTTAGGCCCCACTGTCTTACTGACAATG  
CTTCTCTGCCAACGAGGATGCCCTAAGGGCTGAGGTGTGAAGGCAAATGGTATATTGTA  
ATCTCAGAAATTACAGGAGATACCCCTAAGTATATCTGCTGGTGCCTAGGTTGTCCTCGCT  
ATAACAGCCTCAAAAACCTAAGTATAATCAATTAAAGGGCTCAACCAGCTCACCTGGCTATAC  
CTTGACCATAACCATATCAGCAATATTGACGAAAATGCTTTAATGGAATACGCAACTCAAAGA  
GCTGATTCTTAGTCCAATAGAATCTCTATTCTTAACAATACCTTCAGACCTGTGACAATT  
TACGGAACCTGGATCTGCTATACTAGCTGCATTCTGGGATCTGAACAGTTGGGGCTTG  
CGGAAGCTGCTGAGTTACATTACGGCTAACTCCCTGAGAACCATCCCTGTGCGAATATTCCA  
AGACTGGCGAACCTGGAACCTTGGACCTTGGGATATAACCGGATCGAAGTTAGCCAGGAATG  
TCTTGCTGGCATGACTCAAGAACATTACCTGGAGCACAATCAATTCTCAAGCTCAAC  
CTGGCCCTTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGGAAATAATCAGTGT  
CATAGGACAGACCATGTCCTGGACCTGGAGCTCCTACAAAGGCTTGTATTATCAGGAATGAGA  
TCGAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCGAATCTGAGCGCCTAACCTGGAT  
TCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACATCAG  
TCTTGCTGGAAATATGGGAATGAGCAGAAATATTGCTCCCTGTAACACTCGCTGAAAGTT  
TTAAAGGTCAAGGGAGAATACAATTATCTGTCAGTCCCAAAGAGACTGCAAGGAGATAATGTG  
ATCGATGCAGTGAAGAACTACAGCATCTGTCAGTCCCAAAGACTCCTGGAGCTGCAAGGAGATAATGTG  
GGCTCTCCCAAAGCGACGTTAACGCCAAGCTCCCCAGGGCGAACGATGAGGACAACCCCT  
TGCCCCCGACGGTGGAGCCACAGAGGCCGCCCCAGAGAACCGATGTCAGGCCGAGCACATCT  
TTCCATAAAATCATCGCGGGCAGCGTGGCCTTCTGTCGTGTCATCCTGCTGGTTAT  
CTACGTTGTCATGGAGCGGTACCCCTGCGAGCATGAAGCAGCTGAGCGCAGCGCTCCCTCATGCGAA  
GGCACAGGAAAAGAAAAGACAGTCCCTAACGAAATGACTCCAGCAGGACCCAGGAATTATGTA  
GATTATAAACCCACCAACACGGAGAGACCGAGATGCTGAATGGACGGGACCCCTGCACCTA  
TAACAAATCGGGCTCCAGGGAGTGTGAGGTATGAACCTTGTGATAAAAAGAGCTTAAAGCT  
GGGAAATAAGTGGTGTATTGAACTCTGGTACTATCAAGGGAACGCGATGCCCTCCCTCCCC  
TTCCCTCTCCCTCACTTTGGTGGCAAGATCCCTGTCGTTAGTGCATTATAACT  
GGTCATTTCTCTCATACATATAACCCATTGAAATTAAATACCAACATCAATGTGAAGCTT  
GAACCTCGGTTAATATAACCTATTGTATAAGACCTTACTGATTCCATTAAATGTCGCAATT  
GTTTAAGATAAAACTCTTCTAGTAAAAAA

## **FIGURE 124**

MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMYCESQKLQEIPSSISAGCLG  
LSLRYNSQLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLNNTR  
PVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHRSNSLRTIPVRIQDCRNLELLDLGYNRIRS  
LARNVFAGMIRLKELHLEHNQFSKLNLAFFPRLVSLQNLQWNKISVIGQTMSTWSSLQRLDL  
SGNEIEAFSGPSVFQCVPNLQRLNLDNSKLTFIGQEILDWSWISLNDISLAGNIWECSRNICSLVN  
WLKSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLARALPKPTFKPKLPRKHE  
SKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVIIVSWKRYPASMKQLOQR  
SLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLNGTGPCTYNKSGSRECEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

## **FIGURE 125**

CCGTTATCGTCTTGCCTACTGCTGAATGTCGTCCCAGGAGGAGGAGGCTTGTCCGCTG  
ACCCAGAGATGGCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGCTACCGTGGCGAGCT  
AGCAACCTTCCCTGGATCTCACAAAACCTGACTCCAAATGCAAGGAGAAGCAGCTTGCTC  
GGTGGGAGACGGTGCAGAGAAATCTGCCCCCTATAGGGGAATGGTGCACAGCCCTAGGGATC  
ATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGCACCCGCCATTACAGACACGTAGT  
GTATTCTGGAGGTGCAATGGTCACATATGAACATCTCCGAGAGGTTGTGTTGGCAAAAGTGAAG  
ATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATGGCTGGTGTATTGGCAGTT  
TTAGCCAATCCAACGTGACCTAGTGAAGGTTAGATGCAAATGGAAGGAAAAGGAAACTGGAAGG  
AAAACCATTGCGATTCGTGGTGTACATCATGCATTGCAAAATCTAGCTGAAGGAGGAATAC  
GAGGGCTTGGCAGGCTGGTACCCAAATACAAAGAGCAGCACTGGTAATATGGGAGATTAA  
ACCACTTATGATACTGAAACACTACTTGGTATTGAATACACCACCTGAGGACAATATCATGAC  
TCACGGTTATCAAGTTATGTTCTGGACTGGTAGCTCTATTCTGGAACACCAGCGATGTCA  
TCAAAAGCAGAATAATGAATCAACCACGAGATAAACAAAGGAAGGGACTTTGTATAATCATCG  
ACTGACTGCTTGATTCAAGGTGAAGGATTGAGTCTATATAAAGGCTTTTAC  
ATCTTGGCTGAGAATGACCCCTGGTCAATGGTGTCTGGCTACTTATGAAAAAATCAGAGAGA  
TGAGTGGAGTCAGTCCATTTAA

## **FIGURE 126**

MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGARES  
APYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLREVVFGKSEDEHYPLWKS  
VIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHAFAKILAEGGIRGLWAGWVP  
NIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTPADVIKSrimnQP  
RDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLTYEKIREMSGVSPF

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

## **FIGURE 127**

CGCGGATCGGACCAAGCAGGTGGCGGCGGCAGGAGAGCGGCCGGCGTCAGCTCCTCGAC  
CCCCGTGTCGGGCTAGTCCAGCGAGGCGACGGCGGCGTGGGCCATGGCCAGGCCGGCATGG  
AGCGGTGGCGCGACCGCTGGCGCTGGTACGGGGCCTCGGGGGCATCGGCAGGCCGTGGCC  
CGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGCTGCAGCCGCACGTGGCAACATCGAGGA  
GCTGGCTGCTGAATGTAAGAGTCAGGCTACCCGGACTTGTACAGATGTGACCTAT  
CAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATC  
TGCATCAACAATGCTGGCTTGGCCGGCCTGACACCCCTGCTCTCAGGCAGCACCGAGTGGTGGAA  
GGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGAAAGCCTACCGAGTCCATGA  
AGGAGCGGAATGTGGACGATGGCACATCATTAACATCAATAGCATGCTGGCCACCGAGTGTAA  
CCCCTGTCGTGACCCACTTCTATAGGCCACCAAGTATGCCGTACTGCCGTGACAGAGGGACT  
GAGGCAAGAGCTCGGGAGGCCAGACCCACATCCGAGGCCACGTGCATCTCCAGGTGTGGTGG  
AGACACAATTGCCCTCAAACCTCACGACAAGGACCTGAGAAGGCAGTGCACCTATGAGCAA  
ATGAAGTGTCTCAAACCGAGGATGTGGCCAGGGCTGTATCTACGCTCAGCACCCCCGACA  
CATCCAGATTGGAGACATCCAGATGAGGCCACGGAGCAGGTGACCTAGTGAATGTGGAGCTCC  
TCCTCCCTCCCCACCCCTCATGGCTGCCCTGCCTCTGGATTAGGTGTTGATTTCTGGAT  
CACGGGATACCACTCCTGTCCACACCCCGACCAGGGCTAGAAAATTGTTGAGATTTTATA  
TCATTTGTCAAATTGCTTCAGTTGTAATGTGAAAAATGGCTGGGAAAGGAGGTGGTGTCCC  
TAATTGTTTACTTGTAACTTGTCTTGCCCCCTGGGACTTGGCTTGTGCTCTCAGTG  
TCTTCCCTTGACATGGAAAGGAGTTGTGGCCAAATCCCCATCTTGCACCTCAACGTCTG  
TGGCTCAGGGCTGGGTTGGCAGAGGGAGGCCACCTCACCTTATCTGTGTTGTTATCCAGGGCTCC  
AGACTTCCCTCTGCCCTGCCCCACTGCACCCCTCTCCCCCTATCTATCTCCTCTCGGCTCCCC  
AGCCCAGTCTGGCTTGTCCCCCTGGGGTACCCCTCACTCTGACTCTGACTATGGCAG  
CAGAACACCAGGGCTGGCCAGTGGATTGATGGTACATTTGAGATTTGAGATTTGAGATTTGAG  
AAAAAAA

## **FIGURE 128**

MARPGMERWRDRLALVTGASGGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGYPGTLI  
PYRCDLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNLALSICTR  
EAYQSMKERNVDDGHIININMSGHRLPLSVTHFYSATKYAVTALTEGLRQELREAQTHIRATC  
ISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQMRPTEQVT

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-myristoylation sites.**

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,  
199-205

**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

## **FIGURE 129**

AACTTCTACATGGGCTCCTGCTGGTGCCTCCCTCAGCCTCTGCCGGTGCCTACACCAT  
CATGTCCCTCCACCTCCTTGACTGCGGGCCGTTCAGGTGCAGAGTCTCAGTTGCCGGAGC  
ACCTCCCCCTCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCAGAATTCCAGTTCTGGTTTATGC  
CAGCCTGTAAAAGGCCATGGAACTTGGTGAATCACCGATGCCATTAAAGAGGGTTTCTGCCA  
GGATGGAAATGTTAGGTCGTTCTGTCTGCCTGTTCAATTTCAGTAGCCACCAGCCACCTGTGG  
CCGTTGAGTGCTTGAAAATGAGAACTGAGAAAATTAAATTCTCATGTATTTCATTTATTAA  
TTAATTAACTGATAGTTGTACATATTGGGGTACATGTGATATTGGATACATGTATAACAA  
TATATAATGATCAAATCAGGGTAACGGGATATCCATCACATCAAACATTATTTCATTCTT  
TTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGGTGCATCTCAGCTTACTGCAAC  
CTCTGCCCTGCCAGGTTCAAGCGATTCTCATGCCCTCACCTCCAAAGTAGCTGGACTACAGGCAT  
GCACCCACAATGCCCAACTAATTGGTATTAGAGACGGGGTTTGCATGTTGCCAGG  
CTGGCCTTGAACTCTGGCTCAAACAACTTGCCTCGGCCTCCAAAGTGTATGATTACA  
GGCGTGAGCCACCGTGCCTGGCTAAACATTATCTTGTGTTGGAACTTGAATTAT  
ACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTCCCTCT  
ATCTAACTGTATATTGTACCAGTTAACCAACCGTACTCTCATCCCCACTCCTCTATCCTTCCCC  
AACCTCTGATCACCTCATTCTACTCTACCTCCATGAGATCCACTTTTAGCTCCACATGTG  
AGTAAGAAAATGCAATATTGTCCTTCTGCGCTGGTATTCACTTAAACATAATGACTTCCTG  
TTCCATCCATGTTGCTGCAAATGACAGGATTGCTTAATTCAATTAAAATAACCACACATG  
GCAAAAAA

## **FIGURE 130**

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRSVAREHLPGRGSLLRGPRPRIPVLVSCQPV  
KGHGTLGESPMMPFKRVFCQDGTVRSFCVCAVFSSHQPPVAVECLK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 86-92

**Zinc carboxypeptidases, zinc-binding region 2 signature.**

amino acids 68-79

## **FIGURE 131**

TTCTGAAGTAACGGAAGCTACCTTGATAAAGACCTAACACTGCTGACCATGATCAGCGCAGCCTGGAGC  
ATCTTCCTCATCGGGACTAAAATTGGGCTGTTCTCAAGTAGCACCTCTATCAGTTATGGCTAAATCCCTG  
TCCATCTGTGTGCGCTGCGATGCGGGTTTCATTACTGTAATGATCGCTTCTGACATCCATTCAAACAG  
GAATACCAGAGGATGCTACAACTCTACCTCAGAACAAACAAATAATGCTGGATTCCCTCAGAT  
TTGAAAAACTTGCTGAAAGTAGAAAGAATATACTATACCAACAGTTAGATGAATTCCCTACCAACCT  
CCCAAAGTATGAAAGAGTTACATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTCAA  
AAATTCCCTATCTGGAAGAATTACATTTAGATGACAACCTGCTCTGCAGTTAGCATAGAAGAGGGAGCA  
TTCCGAGACAGCAACTATCTCGACTGCTTTCTGTCGGTAAACCTACCTAGCACAATTCCCTGGGTT  
GCCAGGACTATAGAAGAACTACGCTGGATGATAATCGCATATCCACTATTCATCACCATCTCTCAAG  
GTCTCACTAGTCTAAACGCCTGGTCTAGATGAAACACTGTTGAACAATCATGGTTAGGTGACAAGTT  
TTCTTCACCTAGTTAATTGACAGAGCTGTCCTGGTGCAGAATTCCCTGACTGCTGACCAAGTAAACCT  
TCCAGGCACAAACCTGAGGAAGCTTATCTCAAGATAACCACATCAATCGGGTCCCCAAATGCTTTT  
CTTATCTAAGGCAGCTATCGACTGGATATGCTAACATAACCTAACCTAACGTAATTACCTCAGGGTATCTT  
GATGATTGGACAATATAACACAACGATTCTCGAACAAATCCCTGGTATTGCGGGTCAAGATGAAATG  
GGTACGTAACGGTTACAATCACTACCTGTGAAGGTCAACCGTGCCTGGGCTCATGTGCCAACCCCCAGAAA  
AGGTTGGTGGATGGCTATTAAGGATCTAACGAAACTGTTGATTGTAAGGACAGTGGGATTGTAAGC  
ACCATTCAAGATAACCACGCAATACCCAAACACACTGATCTGCCAACGGACAGTGGCCAGCTCAGTGAC  
CAAACAGCCAGATATTAAGAACCCAAAGCTCAACTAACGATCAACAAACCAAGGGAGTCCCTCAAGAAAAAA  
CAATTACAATTACTGTGAAGTCTGCACCTGTACATACCATTCAATCTCTGGAAACTGCTCTACCTATG  
ACTGCTTGAGACTCAGCTGGTTAAACTGGCCATAGCCCCGCAATTGGATCTATAACAGAAACAATTGT  
AACAGGGGAACGCAACTCTACCTTACCTATTGATGAAACTCCTGGTATTGAGACTGAAACTGCACCCCT  
CCATGGAAACCAAGCAACCTCTACCTATTGATGAAACTCCTGGTATTGAGACTGAAACTGCACCCCT  
CGAATGTACAACCCCTACAACCACCCCTAACATCGAGAGCAAGAGAAAGAACCTAACAAACCCAAATTAC  
TTGGCTGCCATCTGGTGGGGCTGTGGCCCTGGTTACCATGGCTTCTGCTTGTGTTGGTATG  
TTCATAGGAATGGATCGCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAAAGGATGACTAT  
GCAGAAAGCTGGCACTAACGAGGACAACCTATCCTGGAAATCAGGGAAACTCTTCAAGATGTTACCAAT  
AAGCAATGAACCCATCTGAAGGAGGAGTTGTAATACACCCATATTCCCTCTAACGGATGAATCTGT  
ACAAAAACAAATCACAGTGAAGCAGTAGTAACCGAAGCTACAGAGACAGTGGTATTCCAGACTCAGATCAC  
TCACACTCATGATGCTGAAGGACTCACAGCAGACTTGTGTTGGTTTTAACCTAAGGGAGGTGATG  
GT

## **FIGURE 132**

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCNDRFLTSIPTGIPEDATTLYL  
QNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLSKIPYL  
EELHLDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSI PWGLPRTIEELRLDDNRISTISSPSL  
QGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKLYLQDNHIN  
RVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDLDNITQLILRNNPWC GCKMKWV RDWLQSLPV  
KVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQTIA PNTVPAQGQWPAPVTKQPD  
IKNPKLTKDQQTTGSPSRKTITITVKS VTS DTIHISWKLALPMTALRLS WLKLGHSPAFGSITET  
IVTGERSEYLVTALEPDSPYKCMVPMETS NLYLFDETPVCIETETAPLRMYNPTTLNREQEKE  
PYKPNPLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSKGRRKDDYAEAGTKKD NS  
ILEIRETSFQMLPISNEPISKEE FVIHTIFPPNGMNLYKNNHSESSSNRSYRDSGIPDSDHSHS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 531-552

**N-glycosylation sites.**

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

**Tyrosine kinase phosphorylation site.**

amino acids 515-522

**N-myristoylation sites.**

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,

640-645

**Amidation site.**

amino acids 567-570

**Leucine zipper pattern.**

amino acids 159-180

**Phospholipase A2 aspartic acid active site.**

amino acids 34-44

### **FIGURE 133**

CCGTCACTCCCCCTGCAGCCACCCCTCCCAGAGTCCTTGCCCAGGCCACCCAGGCTTCTGGCA  
GCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGAGGTGGGAAGGAGGTGGGAGGAGGGCG  
TGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGAGCAGAG  
GCCGGCCATGGCCAGCCTGGGCTGCTGCTCTGCTTACTGACAGCACTGCCACCGCTGTGGT  
CCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACACTGATCCTGTCT  
GCGCTGGAGAGAGCCACCGTCTCCTAGAACAGAGGCTGCCTGAAATCAACCTGGATGGCATGGT  
GGGGGTCCAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGCCAGGAGCCCTGC  
TGCAGCCGCTGAGCCTGCGCTGGGATGCTGGGGAGAAGCTGGAGGCTGCCATCCAGAGATCC  
CTCCACTACCTCAAGCTGAGTGATCCAAAGTACCTAACAGAGAGTCCAGCTGACCCCTCAGCCCG  
GTTTGAAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTGGTGTACCCACGTTGGC  
CCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGCGCTGGTGCAGCTGCTGGAACCGGGACG  
GACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAGCCTCATGACCAAGCCGGCTGCTC  
AGGCTACTGCCTGTCACCAACTGCTCTTCCCTGGGAGAATGAGGGATGCACACAGG  
GACCACCTCAACAGAGCCAGGACTATATCAACCTCTGCGCCACATGATGGACTTGAAACCG  
AGAGCTGAGGCCATGGATACGCCTACCCCTACCGGGACATCTCATGGAAAACATCATGTTCTG  
TGGAAATGGGGGGCTCTCCGACTTCTACAAGCTCCGGTGGCTGGAGGCCATTCTCAGCTGGCAGA  
AACAGCAGGAAGGATGCTCGGGGAGCCTGATGCTGAAGATGAAGAATTATCTAAAGCTATTCAA  
TATCAGCAGCATTTCGAGGGAGGTGAAGAGGCAGAAAAAACATTCCAGATTCTCGCTCTGT  
TGCTCAGGCTGGAGTACAGTGGCGCAATCTGGCTCACTGCAACCTTGCCCTGGTTCAAGC  
AATTCTTGCCTCATCCTCCGAGTAGCTGGACTACAGGAGCGTGCACCATCTGGCTAAT  
TTTATATTTTTAGAGACAGGGTTCATCATGTTGCTCATGCTGGTCTCGAACCTCTGAT  
CTCAAGAGATCCGCCACCTCAGGCTCCAAAGTGTGGATTATAGGTGTGAGCCACCGTGTCTG  
GCTGAAAAGCACTTCAAAGAGACTGTGTTGAATAAAGGGCCAAGGTTCTGCCACCCAGCACTC  
ATGGGGCTCTCCCTAGATGGCTGCTCTCCACAAACACAGCCACAGCAGTGGCAGCCCTGG  
GTGGCTCCTATACATCCTGGCAGAATACCCCCCAGCAAACAGAGGCCACACCCATCCACACCG  
CCACCCACCAAGCAGCGCTGAGACGGACGGTCCATGCCAGCTGCCCTGGAGGAGGAACAGACCC  
TTAGTCCTCATCCCTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGG  
ATAAGCAAAGCCACCCGACACCCAAATCTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGG  
GGCCGGGAGGGACCCAGGTGTGAACGGATGAATAAGTCACACTGCAACTGCAACTGAAAAAAA

## **FIGURE 134**

MSARGRWEGGGRRACRGSGLARAQGAERVTSSEQRPMASLGLLLLLTLAPPLWSSSLPGLD  
TAESKATIADLILSALERATVFQRLPEINLDGMGVVRVLEEQLKSVREKWAQEPLLQPLSLRV  
GMLGEKLEAAIQRSLHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQDSFSEE  
RSDVCLVQLLGTGTDSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQGPLQQSQD  
YINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILSWQKQQEGCFG  
EPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLPPGFQFSCLILP  
SSWDYRSVPYLANFYIFLVETGFHHVAHAGLELLISRDPPTSGSQSVGL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 39-56

**Tyrosine kinase phosphorylation sites.**

amino acids 149-156, 274-282

**N-myristoylation sites.**

amino acids 10-16, 20-26, 63-69, 208-214

**Amidation site.**

amino acids 10-14

**Glycoprotein hormones beta chain signature 1.**

amino acids 230-237

## **FIGURE 135**

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGCTTCTTCCGTCTGCTGCTG  
CTGCTGCTATCGGGGATGTCCAGAGCTGGAGGTGCCGGGCTGCTGCTGAGGGATCGGGAGG  
GAGTGGGGTCGGCATAGGAGATCGCTCAAGATTGAGGGCGTAGCTGAGCAGGGTGAAGC  
CTCAGGACTGGATCTCGCGGCCGAGTGTGGTAGACGGAGAAGAGCACGTCGGTTCTTAAG  
ACAGATGGAGTTGTGGTTCATGATATACTTCTGGATCTTATGTAGTGGAAAGTTGTATCTCC  
AGCTTACAGATTTGATCCCGTTGAGTGGATATCACTTCGAAAGGAAAATGAGAGCAAGATAG  
TGAATTACATAAAACATCAGAGGTTGTCAAGCTGCCCTATCCTCTCCAAATGAAATCTCAGGT  
CCACCTTCTTACTTTATTAAAAGGAATCGTGGGCTGGACAGACTTCTAATGAACCCAATGGT  
TATGATGATGGTTCTCCTTATTGATATTGTGCTCTGCCTAAAGTGGTCAACACAAGTGATC  
CTGACATGAGACGGAAATGGAGCAGTCAATGAATATGCTGAATTCCAACCATGAGTTGCCTGAT  
GTTTCTGAGTTCATGACAAGACTCTCTCTCAAAATCATCTGGCAAATCTAGCAGCGGCAGCAG  
TAAAACAGGCAAAAGTGGGCTGGCAAAAGGAGGTAGTCAGGCCGTCCAGAGCTGGCATTGCAC  
AAACACGGCAACACTGGGTGGCATCCAAGTCTGGAAAACCGTGTGAAGCAACTACTATAAAACTT  
GAGTCATCCCGACGTTGATCTTACAACGTGTATGTT  
AACTTTTAGCACATGTTGTACTTGGTACACGAGAAAACCCAGCTTCATCTTGCTGTAT  
GAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAATTAT  
ATGAACACTACATTATGTATATTAAATTAAAACATCTTAATCCAGAAATCAAAAAAAAAAAAA  
AAAAAAAAAAAAAAA

## **FIGURE 136**

MAAALWGFFPVLLLLLSDVQSSEVPGAAEGSGSGVGIGDRFKIEGRAVPGVKPQDWISAA  
RVLVDGEEHVGFLLKTDGSFVVHDIPSGSYVVEVVS PAYRFDPVRVDITSKGKMRARYVNYIKTSE  
VVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMMVLPLLIFVLLPKVVNTSDPDMRREME  
QSMNMLNSNHELPDVSEFMTRLFSSKGSSGSSKTGKSGAGKRR

**Important features of the protein:**

**Signal sequence:**

amino acids 1-23

**Transmembrane domain:**

amino acids 161-182

**N-glycosylation site.**

amino acids 184-187

**Glycosaminoglycan attachment sites.**

amino acids 37-40, 236-239

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 151-154

**N-myristoylation sites.**

amino acids 33-38, 36-41, 38-44, 229-234

**Amidation site.**

amino acids 238-241

**ATP/GTP-binding site motif A (P-loop).**

amino acids 229-236

## **FIGURE 137**

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCTCCCCAGTTCCCTGTGGGTCTGAGGGGA  
CCAGAAGGGTGAGCTACGTTGGCTTCTGAAAGGGGAGGCTATATGCGTCAATTCCCCAAACAA  
GTTTGACATTCCCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCTGTTCCAGGC  
CTTACCTGCTGGGCACTAACGGCGAGCCAGGATGGGACAGAATAAGGAGCCACGACCTGTGC  
CACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTTCACGGGAGGCTTGGCAGT  
TTTCTTACTCCTGTGGCTCCAGATTCAGGCCTAAGATGAAAGCCTCTAGTCCTGCCTTCAGC  
CTTCTCTGCTGCGTTTATCTCCTATGGACTCCTTCACTGGACTGAAGACACTCAATTGGG  
AAGCTGTGTGATGCCACAAACCTCAGGAAATACGAAATGGATTTCTGAGATAACGGGCAGTG  
TGCAAGCCAAGATGAAACATTGACATCAGAAATCTAAGGAGGACTGAGTCCTGCAAGACACA  
AAGCCTGCGAATCGATGCTGCCCTGCGCCATTGCTAAGACTCTATCTGGACAGGGTATTAA  
AAACTACCAGACCCCTGACCATTAACTCTCCGGAAGATCAGCAGCCTCGCCAATTCTTCTTA  
CCATCAAGAAGGACCTCCGGCTCTCATGCCACATGACATGCCATTGTGGGAGGAAGCAATG  
AAGAAATACAGCCAGATTGAGTCACTTGAAAAGCTGAAACCTCAGGCAGCAGTGTGAAGGC  
TTTGGGGAACTAGACATTCTCTGCAATGGATGGAGGAGACAGAATAGGAGGAAAGTGTGCTG  
CTGCTAAGAATATTGAGGTCAAGAGCTCAGTCTCAATACCTGCAAGAGGAGGATGACCCAA  
ACCACCATCTTACTGTACTAGTCTGTGCTGGTCACAGTGTATCTTATTGCTATTACTTG  
CTTCCTTGCATGATTGTCTTATGCATCCCCAATCTTAATTGAGACCATACTTGCTATAAGATT  
TGTAATATCTTCTGCTATTGGATATATTATTAGTTAATATATTATTATTGCTATT  
ATGTATTATTTTTACTTGGACATGAAACTTAAAAAAATTACAGATTATTTATAACCTG  
ACTAGAGCAGGTGATGTATTGACTACTTAGGATGGGTTGGAATAAGTTTGATGTGAAATTGCAC  
CTAGGGGGTTATTCAATTGACTAAGGACATATTACTCATGCTGATGCTCTGTGAGAT  
ATTGAAATTGAACCAATGACTACTTAGGATGGGTTGGAATAAGTTTGATGTGAAATTGCAC  
ATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATATTGTGTATCTCCAG  
CCAGGAATCCTACACGGCCAGCATGATTCTACAAATAAGTTCTTGCATACCAAAAAAAA  
AAAAAAAAAAA

## **FIGURE 138**

MRQFPKTSFDISPEMSFSIYSLQVPAVGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPEIF  
SSREAWQFFLLLWSPDFRPKMASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQEIRNG  
FSEIRGSVQAKDGNIDIRILRRTESLQDTK PANRCCLRHLLRLYLDdrvFKNYQTPDHYTLRKIS  
SLANSFLTIKKDLRLSHAHMTCHGEEAMKKYSQILSHFEKLEPQAAVVKALGELDILLQWMEET  
E

**Important features of the protein:**

**Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

## **FIGURE 139**

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCGCATCCAGCC  
TAGCGTGTCCACCGATCGGGCTGGGCTCCGGACTTCGCTACCTGTGCGTAGCGATCGAGGTGC  
TAGGGATCGCGGTCTTCCTCGGGATTCTCCCGGCTCCCGTCCGTTCTGCCAGAGCGGAA  
CACGGAGCGGAGCCCCAGCGCCCGAACCCCTCGGCTGGAGCCAGTTCAACTGGACCACGCTGCC  
ACCACCTCTTCAGTAAAGTTGTTATTGTCTGATAGATGCCCTGAGAGATGATTTGTGTTG  
GGTCAAAGGGTGTGAAATTATGCCCTACACAACCTACTTGTGAAAAGGAGCATCTCACAGT  
TTTGTGCTGAAGCAAAGCCACCTACAGTTACTATGCCCTGAATCAAGGCATTGATGACGGGGAG  
CCTTCCTGGCTTGTGACGTACAGAACCTCAATTCTCTGCACTGCTGGAAGACAGTGTGA  
TAAGACAAGCAAAGCAGCTGAAAAGAAATAGTCTTTATGGAGATGAAACCTGGGTTAAATTA  
TTCCCAAAGCATTGTGGAATATGATGGAACAACCTCATTTCGTGTCAGATTACACAGAGGT  
GGATAATAATGTACGAGGCATTGGATAAAGTATTAAAAAGAGGGAGATTGGGACATATTAATCC  
TCCACTACCTGGGGCTGGACCACATTGGCACATTTCAGGGCCAACAGCCCCCTGATTGGGAG  
AAGCTGAGCGAGATGGACAGCGTGTGATGAAGATCCACACCTCACTGCACTGAGCTGAAGGGAGAGA  
GACGCCCTTACCCATTGCTGGTTCTTGTTGACCATGGCATGTCGAAACAGGAAGTCACG  
GGGCCTCCTCCACCGAGGGAGGTGAATACACCTCTGATTAACTCAGTTCTGCGTTGAAAGGAAA  
CCCGGTGATATCCGACATCCAAGCACGTCCAATAGACGGATGTGGCTGCGACACTGGCAGTAGC  
ACTTGGCTTACCGATTCCAAAAGACAGTGTAGGGAGCCTCTATTCCAGTTGTGGAAGGAAGAC  
CAATGAGAGAGCAGTTGAGATTTCATTTGAATACAGTGCAGCTAGTAAACTGTTGCAAGAG  
AATGTGCCGTATGAAAAAGATCCTGGGTTGAGCAGTTAAATGTCAGAAAGATTGCAATTGG  
GAACTGGATCAGACTGTACTTGGAGGAAAAGCATTCAAGAGTCTATTCAACCTGGCTCCAAGG  
TTCTCAGGCAGTACCTGGATGCTCTGAAAGACGCTGAGCTTGTCCCTGAGTGACAAAGTGGCCAG  
TTCTCACCTGCTCTGCTCACAGCTCCACAGGCACTGCACAGAAAGGCTGAGCTGGAAGTCCA  
CTGTCATCTCCTGGTTTCTGCTCTTATTGGTATCCTGTTCTTCCGGCGTTACGT  
CATTGTGTGCACCTCAGCTGAAAGTTCGTGCTACTTCTGTTGCTCTGAGTGACAAAGTGGCCAG  
GCCTTCGTTACCAAGACTCTGGTTGAACACACTGGTGTGCCAAGTGCTGGCAGTGCCCTGGAC  
AGGGGGCTCAGGGAAAGGACGTGGAGCAGCTTATCCCCAGGCTCTGGGTGTCCCACACAGGTG  
TTCACATCTGTGCTGTCAGGTCAAGTGCCTAGTTCTGAAAGCTAGGTTCTGCGACTGTTAC  
CAAGGTGATTGTAAGAGCTGGCGGTACAGAGAACAGAACAGCTGAGGGGGTGTGTGAA  
TCGGACAGCCTCCACAGCAGAGGTGTGGGAGCTGAGCTGAGGGAGAACAGAACATGGCCTGGA  
CACTCAGGAGGGTCAAAAGGAGACTTGGTCGACACTCATCTGCCACCCCCAGAACATGCATCCT  
GCCTCATCAGGTCCAGATTCTTCCAAGGGCGACGTTCTGTTGGAATTCTTAGTCCTGGCC  
TCGGACACCTCATCTGTTAGCTGGGGAGTGGTGGTGAAGCAGTGAGAAGAGGGCGATGGTCAC  
ACTCAGATCAGAGGCCAGGATCAAGGGACCCACTGCAGTGGCAGCAGGACTGTTGGCCAG  
ACCCCAACCTGCAACCTCATCCCCCTTGGCTTGAGCCGTCAAGGGCCCTGTGCTGAGTGT  
CTGACCGAGACACTCACASCTTGTACAGGGCACAGGCTTCTCGGAGGCCAGGATGATCTGTG  
CCACGCTTGCACCTCGGGCCATCTGGCTCATGCTCTCTCCTGCTATTGAATTAGTACCTAG  
CTGCACACAGTATGTAGTTACAAAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 140**

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPEPSAGASSNWTLPPPLF  
SKVVIVILIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMTGSLPGF  
VDVIRNLNSPALLEDSVIROAKAAGKRIVFYGDETWVKLFPKHFVEYDGTTSFVSDYTEVDNNV  
TRHLDKVLKRGDWDILILHYLGLDHIGHISGPNSPLIGQKLSEMDSVLMKIHTSLQSKERETPLP  
NLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 58-76

**N-glycosylation sites.**

amino acids 56-60, 194-198

**N-myristylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

**Amidation site.**

amino acids 154-158

**Cell attachment sequence.**

amino acids 205-208

## **FIGURE 141**

GGCACGAGGCAAGCCTTCCAGGTATCGTGACGCACCTTGAAAGTCTGAGAGCTACTGCCCTACAGAAAGTTACTAGTGCCTAAAGCTGGCGCTGGCACTGATGTTTACTGCTGCTGTTGGAGTACAACCTCCCTATAGAAAACAACGCCAGCACCTTAAGACCACCTCACACCTTCAGAGTGAAGAACTTAAACCCGAAGAAATTCAAGCATTCAATGACCAGGATCACAAAGTACTGGTCCTGGACTCTGGGAATCTCATAGCAGTCCAGATAAAAACATACAGCCAGAGATCTTCTTGCAATTAGCCTCATCCTTGAGCTCAGCCTCTGGGAGAAAGGAAGTCCGATTCTCCTGGGGTCTCTAAAGGGAGTTTGTCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTCAGCTGAAGAAGGAGAAACTGATGAAGCTGGCTGCCAAAAGGAATCAGCACGCCGCCCTCATCTTATAGGGCTCAGGTGGCTCCTGGAACATGCTGGAGTCGGCGCTACCCCGGATGGTCATCTGCACCTCTGCAATTGTAATGAGCCTGTTGGGTGACAGATAAATTGAGAACAGGAAACACATTGAATTTCATTCAACCAGTTGCAAAGCTGAAATGAGCCCCAGTGAGGTAGCGAATTAGGAACGCCCTCGCTATTGAACTAATGCTGATAAAACACCAAAACCTGCTCACT

## **FIGURE 142**

MLLLLLEYNFPIENNQHLKTTHTFRVKNLNPKKFSIHQDHKVLVLDGNLIAVPDKNYIRPEI  
FFALASSLSSASAEGSPILLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFI  
FYRAQVGSWNMLESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**  
amino acids 33-36

**N-myristoylation site.**  
amino acids 50-55, 87-92

**Interleukin-1**  
amino acids 37-182

## **FIGURE 143**

CTAGAGAGTATAGGGCAGAAGGATGGCAGATGAGTGACTCCACATCCAGAGCTGCCTCCCTTAA  
TCCAGGATCCTGTCCTCCTGTCCTGTAGGAGTGCCTGTTGCCAGTGTGGGTGAGACAAGTTG  
TCCCACAGGGCTGTCAGCAGATAAGATTAAGGGCTGGGTCTGTGCTCAATTAACTCCTGTGG  
CACGGGGCTGGGAAGAGCAAAGTCAGCGGTGCCTACAGTCAGCACCAATGCTGGCCTGCCGTGG  
AAGGGAGGTCTGTCCTGGCGCTGCTGCTCTCTTAGGCTCCAGATCCTGCTGATCTATGC  
CTGGCATTTCACGAGCAAAGGACTGTGATGAACACAATGTCATGGCTCGTTACCTCCCTGCCA  
CAGTGGAGTTGCTGTCACACATTCAACCAACAGAGCAAGGACTACTATGCCTACAGACTGGGG  
CACATCTGAATTCTGGAAGGAGCAGGTGGAGTCCAAGACTGTATTCTCAATGGAGCTACTGCT  
GGGGAGAACTAGGTGTGGAAATTGAAGAGCACATTGACAACACTGCCATTCCAAGAAAGCACAG  
AGCTGAACAATACTTCACCTGCTTCTCACCATCAGCACCAAGGCCCTGGATGACTCAGTCAGC  
CTCCTGAACAAGACCTGCTGGAGGGATTCCACTGAGTGAAACCCACTCACAGGCTTGTCATGT  
GCTGCTCCCACATTCCGTGGACATCAGCACTACTCTCCTGAGGACTCTCAGTGGCTGAGCAGCT  
TTGGACTTGTGTTATCCTATTTGCATGTGTTGAGATCTCAGATCAGTGTAGTTAGAAAATCC  
ACACATCTGAGCTAATCATGTAGTGTAGATCATTAAACATCAGCATTAAAGAAAAAAAAAAAAA  
AAA

## **FIGURE 144**

MLGLPWKGGLSWALLLLLLGSQILLIYAWHFHEQRDCDEHNVMARYLPATVEFAVHTFNQQSKDY  
YAYRLGHILNSWKEQVESKTVFSMELLGRTRCGKFEDDIDNCHFQESTELNNTFTCFFTISTRP  
WMTQFSLLNKTCLEGFH

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 117-121, 139-143

**N-myristylation site.**

amino acids 9-15

## **FIGURE 145**

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCCATGAGGAAG  
CACCTGAGCTGGTGGCTGGCACTGTCTGCATGCTGCTCTTCAGCCACCTCTGCGGTCCA  
GACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCAGATCA  
CTGAGGCCAGGTGGCTGAGAACCGCCGGAGCCTCATCAAGCAAGGCCAGCTGACATT  
GACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTCCCCGATGGCATCCA  
CTACAACGGCTGCTTGAGGCTAATGTGACCAAGGAGGCATTGTCACCGCTGCATCAATGCCA  
CCCAGGCCGAACCAAGGGGGAGTCCAGAACGCCAGACAACAAGCTCCACCAGCAGGTGCTCTGG  
CGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTGTTGGAGAGGGCGCAGGACT  
TCGGGTACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTGATCTGGCTCATGGTGAAAAT  
AAGCTTGCACGGAGGCTGGCAGTACAGAGCCAGCAGGAGCAAATCCTGGCAAGTGACCCAGCT  
CTTCTCCCCAAACCCACGCGTGTCTGAAGGTGCCAGGAGCGCGATGCACACTCGCACTGCCAA  
TGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCCTGATAGATGGGGACTGTGGCTTCT  
CCGTCACCCATTCTCAGCCCTAGCAGAGCGTCTGGCACACTAGATTAGTAGTAAATGCTTGT  
GAGAAGAACACATCAGGCAGTGCCACCTGCTCACAGTACTTCCAACAACCTTAGAGGTAG  
GTGTATTCCCGTTTACAGATAAGGAAACTGAGGCCAGAGAGCTGAAGTACTGCACCCAGCATC  
ACCAGCTAGAAAGTGGCAGAGCCAGGATTCAACCCCTGGCTGTCTAACCCAGGTTTCTGCTCT  
GTCCAATTCCAGAGCTGTCTGGTGTACTTATGTCTCACAGGGACCCACATCCAAACATGTAT  
CTCTAAATGAAATTGTGAAAGCTCCATGTTAGAAATAATGAAAACACCTGA

## **FIGURE 146**

MRKHLSWWLATVCMLLFSHLASAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRK  
LDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNKLHQQ  
VLWRLVQELCSLKHCFWLERGAGLRTVMHQPVLLCLLALIWLVMVK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 157-171

**N-glycosylation sites.**

amino acids 98-102, 110-114

**Tyrosine kinase phosphorylation site.**

amino acids 76-83

**N-myristoylation sites.**

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

**Amidation site.**

amino acids 62-66

## **FIGURE 147**

GCCTTGGCCTCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCGGTCCAGAGTCATTC  
CCTGATGATTTATAGACTCAAAGAAAACTCATGTTCAGAAGCTCTCTTCTGGCCTCCCT  
CTGTCTTCTTCCCTTTCTTCTTAAATTAGTAGCATCTACTCAGAGTCATGCAAGCTGG  
AAATCTTCATTTGCTTGTCAAGTGGGTAGGTCACTGAGTCTAGTTTATTTTGAATTT  
CAACTTCAGATTCAAGGGGTACATGTGAAGGTTGTTATGAGTATATTGCATGATGCTGAGG  
TTTGGGGT

## **FIGURE 148**

MFRSSLLFWPPLCLLSLFLLILISSIYSESCKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGTCE  
GLFYEYIA

**Important features of the protein:**

**Signal peptide:**

amino acids 1-25

**N-myristoylation site.**

amino acids 62-68

## **FIGURE 149**

GTCTCCGCGTCACAGGAACCTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGAGACTTGAC  
TCCCAGCGCCCCAACCTGCTTATCCCTGACCGTCGAGTGTAGAGATCCTGCAGCCGCCAGTCC  
CGGCCCCCTCTCCGCCAACCCACCCCTCTGGCTCTTCTGTTTACTCCTCTTTATTCA  
ACAAAAGCTACAGCTCCAGGAGCCAGCGCCGGCTGTGACCCAAGCCAGCGTGGAAAGAATGGGTT  
CCTCGGGACCGGCACCTGGATTCTGGTGTAGTGTCCCATTCAAGCTTCCCCAACCTGGAGGAA  
GCCAAGACAAATCTACATAATAGAGAATTAAAGTCAGAAAGACCTTGAATGAACAGATTGCTGAA  
GCAGAAGAAGACAAGATTAAAAAACATATCCTCAGAAAACAAGCCAGGTAGAGCAACTATTCTT  
TGTTGATAACTTGAACCTGCTAAAGCAATAACAGAAAAGGAAAAATTGAGAAAGAAAGACAATCTA  
TAAGAAGCTCCCCACTTGATAATAAGTTGAATGTGGAAAGATGTTGATTCAACCAAGAATCGAAAATG  
ATCGATGATTATGACTCTACTAAAGTGATGGATCATAAATTCAAGATGATCCAGATGGTCTCA  
TCAACTAGACGGGACTCCTTAACCGCTGAAGACATTGTCATAAAATCGCTGCCAGGATTATGAAG  
AAAATGACAGAGCCGTGTTGACAAGATTGTTCTAAACTACTTAATCTGGCCTTATCACAGAAAGC  
CAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTACAAAATTAACTCAAGGAAGCCAAACAA  
TTATGAGGAGGATCCAATAAGCCCACAAGCTGGACTGAGAATCAGGCTGGAAAAATACCAGAGAAAG  
TGACTCCAATGGCAGCAATTCAAGATGGCTTGCTAAGGGAGAAAAGATGAAACAGTATCTAACACA  
TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAACCTACAGTGAAGACAACTTGAGGAACCTCA  
ATATTTCCAAATTCTATGCGCTACTGAAAGTATTGATTCAAGAAAAGCAAAAGAGAAAGAAA  
CACTGATTACTATCATGAAAACACTGATTGACTTGTGAAGATGATGGTGAATATGGAACAATATCT  
CCAGAAGAAGGTGTTCTACCTTGAAACTGGATGAAATGATTGCTCTCAGACCAAAACAAGCT  
AGAAAAAAATGCTACTGACAATATAAGCAAGCTTCCAGCACCCTAGAGAAGAGTCATGAAGAAA  
CAGACAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTGAAAGGATTCCACAAAA  
GATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAACAGAAGCCTATTGGAAGC  
CATCAGAAAAAATATTGAATGGTGAAGAAACATGACAAAAGGAAATAAAGAAGATTATGACCTT  
CAAAGATGAGAGACTTCATCAATAAAACAGCTGATGCTTATGTGGAGAAAGGCATCCTGACAAGGAA  
GAAGCCGAGGCCATCAAGCGCATTATAGCAGCCTGTAAAATGGCAAAAGATCCAGGAGTCTTCAA  
CTGTTTCAAGAAAACATAATATAGCTTAAACACTTCAATTCTGTGATTAAAATTTTGACCCAAGG  
GTTATTAGAAAAGTGTGAATTACAGTAGTTAACCTTACAAGTGGTTAAAACATAGCTTCTCCC  
GTAAAAACTATCTGAAAGTAAAGTTGTATGTAAGCTGAAAAAAAAAAAAAAAAAAA

## **FIGURE 150**

MGFLGTGTWILVLVLPIQAFPKPGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPENPG  
QSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTKSGLDHK  
FQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAE  
VLQKLISKEANNYEEDPNKPTSWTENQAGKIPFKVTPMAAIQDGLAKGENDETVSNTLTLTNGL  
RRTKTYSEDNFEELQYFPNFYALLKSIDSEKEAKEKETLITIMKTLIDFVKMMVKYGTISPEEGV  
SYLENLDEMIALQTKNLEKNATDNISKLFPAPEKSHEETDSTKEEAAKMEKEYGSLKDSTKDD  
NSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKGKGNKEDYDLSKMRDFINKQADAYVEKGILD  
EEAEAIKRIYSSL

**N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

**Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

**N-myristoylation sites:**

amino acids 143-148, 239-244

## **FIGURE 151**

CGGCTCGAGGCTCCGCCAGGAGAAAGGAAACATTCTGAGGGGAGTCTACACCCCTGGGAGCTCAA  
**GATGGT**CTCTGAGTGGGGCGCTGTGCTTCCGAATGAAGGACTCGGCATTGAAGGTGCTTTATCTGC  
ATAATAACCAGCTCTAGCTGGAGGGCTGCATGCAGGAAAGGTATAAAGGTGAAGAGATCAGC  
GTGGTCCCAATCGTGGCTGGATGCCAGCCTGCCCCGTACATCTGGGTGTCAGGGTGGAAAG  
CCAGTGCCTGTCATGGGGTGGGGCAGGAGCCGACTCTAACACTAGAGCCAGTGAACATCATGG  
AGCTCTATCTGGTGCCTAGGAATCCAAGAGCTCACCTCTACCAGGGACATGGGCTCAC  
TCCAGCTCGAGTCGGCTGCCTACCCGGCTGGTCTGTGCACGGCTGAAGCCGATCAGCC  
TGTCACTACCAAGCTTCCCGAGAATGGTGGCTGGAATGCCCATCACAGACTCTACTCC  
AGCAGTGTGACT**TAGG**CAACGTGCCAGAACTCCCTGGCAGAGCCAGCTGGGTGAGGGGT  
GAGTGGAGGAGACCCATGGCGACAATCACTCTCTGCTCAGGACCCCCACGTGACTTAG  
TGGGCACCTGACCACCTGTCTGGTCCAGTTGATAAATTCTGAGATTGGAGCTCAGT  
CCACGGTCTCCCCACTGGATGGTGCACTGCTGTGAAACCTTGTAAAACCATGTGGGTAAA  
CTGGGAATAACATGAAAAGATTCTGTGGGGTGGGGTGGGGAGTGGTGGGAATCATTCTGCT  
TAATGGTAACGTGACAAGTGTACCTGAGCCCCGAGGCAACCCATCCCCAGTGTGACCTTATA  
GGGTCACTAGCTCTCCACATGAAGTCTGTCACTCACCAGTGTGAGGAGAGGGAGTGGTCATA  
GAGTCAGGGATCTATGCCCTGGCCAGCCCCACCCCTTCAATCTGCCACTGTCTATA  
TGCTACCTTCCTATCTTCCCTCATCATTTGTGTTGGCATGAGGAGGTGGTGTGACGAA  
GAAATGGCTCGAGCTAGAAGATAAAAGATAAGTAGGGTATGCTGATCCTTTAAAAACCCAA  
GATACAATCAAATCCCAGATGTTGGTCTCTATTCCCATGAAAAGTGCTCATGACATATTGAGA  
AGACCTACTTACAAAGTGGCATATATTGCAATTATTAAATAAAAGATAACCTATTATATT  
TCTTTATAGAAAAAAAGTCTGAAAGTCTTACTTCATTGCAATTGTCAGGGTGGTGGCAGTAT  
AGGTGATTTCTTTAATTCTGTTAATTCTGTTATCTCTAAATTCTACAATGAAGATGA  
ATTCCCTGTATAAAAATAAGAAAAGAAATTAAATCTGAGGTAAAGCAGAGCAGACATCATCTGTA  
TTGTCCTCAGCCTCACTTCCCAGAGTAATTCAAAATTGAAATCAGGCTCTGCTGTCTGGTGG  
TTGTAGTAGTGTACAGGAAACAGATCTCAGCAAGGCACTGAGGAGGGCTGTGCTGAGTTGT  
GTGGCTGGAATCTGGTAAAGGAACCTAAAGAACAAAATCATCTGTAATTCTTCTAGAAG  
GATCACAGCCCCCTGGGATTCCAAGGCATTGATCCAGTCTCAAGAAGGCTGCTGACTGGTGA  
ATTGTGCTCCCCCTCAAAATTCACATCCTCTGGAATTCTCAGTCTGTGAGTTATTGGAGATAAG  
GTCTCTCAGATGTAGTTAGTAAAGACAAGGTATGCTGGATGAAGGTAGACCTAAATTCAATT  
GACTGGTTCTCTGTATGAAAAGGAGAGGACACAGAGACAGGGAGACGGGGAAAGACTATGTA  
AAGATGAAGGAGAGATCGGAGTTTGCAAGGCAACAGCTAAGAAACACCAAGGATTGTGGCAACC  
ATCAGAAAGCTTGGAGAGGCAAGAAGAATTCTCCCTAGAGGCTTAGAGGGATAACGGCTCTG  
CTGAAACCTTAACTCAGACTTCCAGCCTCTGAACGAGAAAGAATAATTCTGGCTGTTAA  
GCCACCAAGGATAATTGGTACAGCAGCTAGGAAACTAATACAGTGTAAATGATCCCTGT  
CTCCTCGTGTACATTCTGTGTGTCCTCCCACATGTACCAAGATTAGTTATAAAAGACACTGCA  
GAGCTAGCTGCCATGCTATGAGCAGGGCTATAAGAGACTTACGTGTTAAAAAGAAGTCTCT  
GCCACAGCCACATTAGTGAACCTAGAAGCAGAGACTCTGTGAGATAATCGATGTTGTTGTTT  
AAGTTGCTCAGTTGGTCTAACTGTGAGATAATGAGAAAGAGAAGAG

## **FIGURE 152**

MVLSGALCFRMKDSALKVLYLHNNQLLAGGLHAGKVIKGEIISVVPNRWLDASLSPVILGVQGGS  
QCLSCGVGQEP TLLEPVNIMELYLGAKESKSFTFYRRDMGLTSSFESAAYPGWFLCTVPEADQP  
VRLTQLPENGGWNAPITDFYFQQCD

**N-myristoylation sites.**

amino acids 29-34, 30-35, 60-65, 63-68, 73-78, 91-96, 106-111

**Interleukin-1 signature.**

amino acids 111-131

**Interleukin-1 proteins.**

amino acids 8-29, 83-120, 95-134, 64-103

## **FIGURE 153**

CTTCAGAACAGGTTCTCCTCCCCAGTCACCAGTTGCTCGAGTTAGAATTGTCTGCAATGGCCGC  
CCTGCAGAAATCTGTGAGCTTTCTTATGGGACCCGGCCACCAGCTGCCCTCTCTGG  
CCCTCTGGTACAGGGAGGAGCAGCTGCGCCCATCAGCTCCACTGCAGGCTTAGCTGGCTGATAA  
TTCCAGCAGCCCTATATCACCAACCGCACCTCATGCTGGCTAAGGAGGCTAGCTGGCTGATAA  
CAACACAGACGTTCTCATGGGAGAACTGTTCCACGGAGTCAGTATGAGTGAGCGCTGCT  
ATCTGATGAAGCAGGTGCTGAACCTCACCCCTGAAGAAGTGTGCTCCCTCAATCTGATAGGTT  
CAGCCTATATGCAGGGAGGTGGGCCCTCTGGCCAGGCTCAGCAACAGGCTAAGCACATGTCA  
TATTGAAGGTGATGACCTGCATATCCAGAGGAATGTGCAAAAGCTGAAGGACACAGTGAAAAAGC  
TTGGAGAGAGTGGAGAGATCAAAGCAATTGGAGAACTGGATTGCTGTTATGTCTCTGAGAAAT  
GCCTGCATTTGACCAAGAGCAAAGCTGAAAAATGAATAACTAACCCCCCTTCCCTGCTAGAAATAA  
CAATTAGATGCCCAAAGCGATTTTTAACAAAAGGAAGATGGAAAGCCAAACTCCATCATG  
ATGGGTGGATTCCAAATGAACCCCTGCGTTAGTTACAAAGGAAACCAATGCCACTTTGTTATA  
AGACCAGAAGGTAGACTTTCTAAGCATAGATATTATTGATAACATTGTAACTGGTGTTC  
TATACACAGAAAACAATTATTAAATAATTGTCTTTCCATAAAAAAGATTACTTTCCAT  
TCCTTAGGGAAAAACCCCTAAATAGCTCATGTTCCATAATCAGTACTTATATTATAAA  
TGTATTATTATTATTATAAGACTGCATTTATTATCATTAAATTGATTATT  
AGAAACATCATTGATATTGCTACTTGAGTGTAGGCTAATATTGATATTATGACAATAATTAT  
AGAGCTATAACATGTTATTGACCTCAATAAACACTGGATATCCC

## **FIGURE 154**

MAALQKVSSFLMGTLATSCLLLALLVQGGAAPISSHCRLDKSNFQQPYITNRTFMLAKEASL  
ADNNNTDVRLLIGEKLFHGVSMERCYLMQVLFNFTLEEVLFQSDRFQPYMQUEVVPFLARLSNRLS  
TCHIEGDDLHIQRNVQKLKDTVKKLGESGEIKAIGELDLLFMSLRNACI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-33

**N-glycosylation sites.**

amino acids 54-58, 68-72, 97-101

**N-myristoylation sites.**

amino acids 14-20, 82-88

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 10-21

## **FIGURE 155**

GGCTTGCTGAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGT  
CAGTCAGTGCCCGACTTGTGACTGAGTGTGAGTCAGTGCAGCAGCATGTACCGAGGTCACTGCAGAGGGC  
TGCCTGAGGGCTGTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGGCAAGC  
TGCCAGGTTGGGGCTGGGGCAAGTGGAGTGGAGAAACTGGATCCCAGGGGAGGGTGCAGAT  
GAGGGAGCACCCAGATTAGGTGAGGACAGTTCTCTCATTAGCCTTCTACAGGTGGTTGCAT  
TCTTGGCAATGGTCATGGGAACCCACACCTACAGCCACTGGCCAGCTGCTGCCAGCAAAGGG  
CAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACTGTGCCTGTGCCTCCCTAGAGCCTGCTAG  
GCCCAACCGCCACCCAGAGTCCTGTAGGGCCAGTGAAGATGGACCCCTAACAGCAGGGCCATCT  
CCCCCTGGAGATATGAGTTGGACAGAGACTGAAACCGGCTCCCCAGGACCTGTACACGCCCGT  
TGCCTGTGCCCGACTGCGTCAGCCTACAGACAGGCTCCACATGGACCCCGGGCAACTCGGA  
GCTGCTCTACCACAAACCAACAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAAGGGACCCACA  
AGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTTCCTAGCTGTGTGTGCAGGGCCCGT  
GTGATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTGGAAACCTGGAGCCAGGTGTACA  
ACCACTGCCATGAAGGGCCAGGATGCCAGATGCTTGGCCCTGTGAAGTGCTGTCTGGAGCAG  
CAGGATCCCGGGACAGGATGGGGGCTTGGGAAAACCTGCACTTCTGCACATTGAAAAGAG  
CAGCTGCTGCTAGGGCCGCCAGCTGGTGTCTGTCTGCTTGGCCCTGTGAAGTGCTGTCTGGAGCAG  
GTTCTGCCATTCTGGAGGCCACCACTCCTGTCTTCCCTTTCCATCCCCGCTACCTG  
GCCCAGCACAGGCACTTCTAGATATTCCCCCTGCTGGAGAAGAAAAGAGCCCCCTGGTTTATT  
TGTGTTGTTACTCATCACTCAGTGAGCATCTACTTGGGTGCATTAGTGTAGTTACTAGCTT  
TTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATAGAGATTATCCAATAAATAT  
CTTTATTTAAAAATGAAAAA

## **FIGURE 156**

MRERPRLGEDSSLISLFLQVVAFLAMVMGHTHTYSHWPSCCPGQDTSEELLRWSTVPVPPLEPA  
RPNRHPESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNS  
ELLYHNQTVFYRRPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

**Important features of the protein:**

**Signal peptide:**

amino acids 1-32

**N-glycosylation site.**

amino acids 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 127-135

**N-myristoylation sites.**

amino acids 44-50, 150-156

## **FIGURE 157**

CCGGCG**GATG**TCGCTCGTGTGCTAACGCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCC  
GACCGTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAACCC  
CCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACTAGTGTGCAACAGGGACTATTCA  
ATTTGATGAATGTAAGCTGGGTACTCCGGCAGATGCCAGCATCCGCTTGTGAAGGCCACCAA  
GATTTGTGTGACGGCAAAGCAACTTCCAGTCTACAGCTGTGAGGTGCAATTACACAGAGG  
CCTTCCAGACTCAGACCAGACCCCTGGTGGTAAATGGACATTTCTACATCGGCTTCCCTGTA  
GAGCTGAACACAGCTATTCATTGGGCCATAATATTCTTAATGCAAATATGAATGAAGATGG  
CCCTTCCATGTCGTGAATTTCACCTCACCAAGGCTGCCTAGACCACATAATGAAATATAAAAAAA  
AGTGTGTCAAGGCCGAAGCCTGTGGATCCGAACATCACTGCTGTGAAAGAAGATGAGGAGACA  
GTTAGAAGTGAACCTCACACCCTCCCCTGGAAACAGATACTGGCTTATCCAACACAGCAC  
TATCATCGGGTTTCAGGTGTTGAGCCACACCAGAAAGAAACAAACGCGAGCTTCAGTGGTGA  
TTCCAGTGACTGGGATAGTGAAGGTGCTACGGTCAGCTGACTCCATATTCTACTTGTGGC  
AGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCACAAACAGGCGTCCCTTCCCT  
GGATAACAAACAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTGCTGCTCTGCTGGTGGCCA  
CATGGGTGCTGGTGGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCTT  
TCTTACCAACCACACTACTGCCCTTCAATTAAAGGTTCTGTGGTTACCCATCTGAAATATGTTCCA  
TCACACAATTGTTACTTCACTGAATTCTCAAAACCATTGCAGAAGTGAGGTGATCCTTGAA  
AGTGGCAGAAAAGAAAATAGCAGAGATGGTCCAGTGCAGTGGCTGCCACTCAAAGAAGGCA  
GCAGACAAAGTCGCTTCCCTTCCATTGACGTCAACAGTGTGCGATGGTACCTGTGGCAA  
GAGCGAGGGCAGTCCAGTGAGAACTCTCAAGACCTCTCCCCCTGCCTTAACCTTCTGCA  
GTGATCTAAGAAGCCAGATTCTGACAAATACGTGGTGGCTACTTAGAGAGATTGATACA  
AAAGACGATTACAATGCTCTCAGTGTCTGCCCAAGTACCCACCTCATGAAGGATGCCACTGCTT  
CTGTGCAAGAACTTCTCCATGTCAAGCAGCAGGTGTCAGCAGGAAAAGATCACAAGCCTGCCACG  
ATGGCTGCTGCTCCTTGT**AG**

## **FIGURE 158**

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTSVATGDYSILMNWSW  
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP  
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKNEETVEVNFTTPLGNRYMALIQH  
STIIGFSQVFEPHQKKQTRASVVIPTGDSSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVFPFLDNNK  
SKPGGWPLLLLSSLVATWVLVAGIYLMWRHERIKKTSFSTTLLPPIKVLVVPSEICFHHTICYFTEFL  
QNHCRSEVILEKWQKKIAEMGPVQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA  
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQQVSAGKRSQACHD  
GCCSL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-14

**Transmembrane domain:**

amino acids 290-309

**N-glycosylation sites.**

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201 and 283  
- 287

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

**Casein kinase II phosphorylation sites.**

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

**N-myristoylation site.**

amino acids 116-122

**Amidation site.**

amino acids 488-492

## **FIGURE 159**

AGCCACCAGCGAACATGACAGTGAAGACCC~~T~~GCATGGCCAGCCATGGTCAAGTACTTGCTGCT  
GTCGATATTGGGGCTTGCCTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCAAAGTAGGACATA  
CTTTTTCCAAAAGCCTGAGAGTTGCCGCCGTGCCAGGAGGTAGTATGAAGCTTGACATTGGC  
ATCATCAATGAAAACCAGCGCGTTCCATGTCACGTAACATCGAGAGCCGCTCACCTCCCCCTG  
GAATTACACTGTCACTGGGACCCCAACC~~GG~~TACCCCTCGGAAGTTGTACAGGCCAGTGTAGGA  
ACTTGGGCTGCATCAATGCTCAAGGAAAGAACATCTCCATGAATTCCGTTCCATCCAGCAA  
GAGACCTGGTCGTCCGGAGGAAGCACCAAGGCTGCTCTGTTCTTCCAGTTGGAGAAGGTGCT  
GGTGACTGTTGGCTGCACCTGCGTCACCCCTGTCA~~CC~~ACCATGTGCAGTAAGAGGTGCATATCC  
ACTCAGCTGAAGAAG

## **FIGURE 160**

MTVKTLHGPAMVKYLLSILGLAFLSEAAARKIPKVGHFFQKPESCPPVPGGSMKLDIGIINEN  
QRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPIQQETLVV  
RRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHQ

**Signal sequence:**

amino acids 1-30

**N-glycosylation site.**

amino acids 83-87

**N-myristoylation sites.**

amino acids 106-111, 136-141

### **FIGURE 161**

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAGTAGGAGGAGAGTCAGGACTCCCAAG  
ACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGGCCCCCTCTGGAGGCTGAAGAGGGATT  
CAGCCCCCTGCCACCCACAGACACGGGCTACTGGGTGCTGCCCTCTGGGGGGGGCAGCAC  
AGGGCCTAGGCTGGGTGCCACCTGGCACCTAGAAGATGCCGTGCCCTGGTTCTGCTGTCT  
TGGCACTGGGCCGAAGCCAGTGGCTTTCTCTGGAGAGGCTTGTGGGCCCTCAGGACGCTACC  
CACTGCTCTCCGGGCTCTCTGCGCCTCTGGACAGTGACATACTCTGCCCTGCCCTGGGGACAT  
CGTGCCTGCTCCGGGCCGGTGTGGCGCTACGCACCTGCAGACAGAGCTGGTGTGAGGGTGC  
AGAAGGAGACGACTGTGACTCTGTCTCGGTGTGGCTGTCCACTTGGCGTGCATGGCACTGG  
GAAGAGCCTGAAGATGAGGAAAAGTTGGAGGAGCAGCTGACTCAGGGTGGAGGAGCCTAGGAA  
TGCCTCTCCAGGCCAAGTCGTCTCTCCCTCCAGGCCCTACCCACTGCCCGTGCCTCTGC  
TGGAGGTGCAAGTGCCTGCTGCCCTGTGCAAGTTGGTCACTGTGTGGCTCTGTGGTATATGAC  
TGCTTCGAGGCTGCCCTAGGGAGTGAACATCTGGTCTATACTCAGCCCAAGGTACGAGAA  
GGAACCTAACACACACAGCAGCTGCCCTGCCCTGGCTAACGTGTCAGCAGATGGTAC  
ACGTGCATCTGGTTCTGAATGTCCTGTAGGAGCAGCAGCTTCGGCCTCTCCCTGACTGGAA  
GTCCAGGGCCCCCCTAACACCCGGTGGCACAAAACCTGACTGGACCGCAGATCATTACCTTGA  
CCACACAGACCTGGTTCCCTGCCCTGTATTCAAGGTGTGGCCTCTGAAACCTGACTCCGTTAGGA  
CGAACACCTGCCCTTCAGGGAGGACCCCCCGCGCACACCAGAACCTCTGGCAAGCGCCGACTG  
CGACTGCTGACCCCTGCAAGAGCTGGCTGCTGGACGCACCGTGTGCGTGCCTGCCCGCAGAACGGGCACT  
GTGCTGGCGGGCTCCGGTGGGACCCCTGCCAGCCACTGGTCCCACCGCTTCTGGAGAACG  
TCACTGTGGACAAGGTTCTCGAGTTCCCATGTGCAAGGGCACCCCTAACCTCTGTGTTCAAGGTG  
AACAGCTGGAGAAGCTGCAAGCTGCAAGGAGCTGTGGCTGACTCCCTGGGCCCTCTCAAAGA  
CGATGTGCTACTGTGGAGACACGAGGCCCCCAGGACACAGATCCCTGTGCTTGGAAACCCA  
GTGGCTGACTTCACTACCCAGAACGCTTCAAGGGCAGTCGCTGAGTACTGGAGAGTACTTACTA  
CAAGACCTGCACTGAGGCAAGTGTCTGCAAGGAGTACTGGAGGAGCTATGGGGCT  
CCCCATGGACAAATACATCCACAAAGCGCTGGGCCCTCGTGTGGCTGCCCTACTCTTICCG  
CTGCGCTTCCCTCATCCTCTCTCAAAAGGATCACCGCAGGGGGCTGAGGCTTGGTAA  
CAGGACGCTCGCTGGGGCGGGCGCCAGGGGCCGCGCCCTGTGCTCTACTCAGCGATGA  
CTCGGGTTTCAGGCCCTGGTGGCGCCCTGGCGTGGCCCTGTGCCAGCTGCCGCTGCGCTGG  
CCGTAGACCTGTGGAGGCCGTGAACTGAGCGCGCAGGGGCCCTGGCTTGGTTTCAGCCAG  
CGGCGCCAGACCCCTGCAAGGAGGGCGCGTGGTGGCTTGTCTTCTCTCCGGTGCCTGGCCT  
GTGCAAGGAGTGGCTACAGGATGGGTGTCCGGGCCGGCGCACGGCCCGCACGACGCCCTCC  
GCCGCTCGCTCAGCTCGTGTGCCGACTTCTGCAAGGGCCGGCGCCGGCAGCTACGTGGGG  
GCCCTGCTTCAGCAGGGCTGCTCACCCGAGCCGTACCCGCCCTTTCGCAAGCGTGCCCT  
CACACTGCCCTCCCAACTGCAAGACTTCTGGGGCCCTGCAAGCAGCTCGCGCCCGCGTTC  
GGCGGCTCCAAGAGAGAGCGAGCAAGTGTCCCGGGCCCTCAGCCAGCCCTGGATAGCTACTTC  
CATCCCCGGGACTCCCGCGCCGGACGCCGGGGTGGGACCAGGGGCCGGACCTGGGGCGGG  
CGGGACTAAATAAGGAGCAGCGCTGTTTCTAAAAAAA

## **FIGURE 162**

MPVPWFILLSLALGRSPVVLSLERLVGPQDATHCSPGLSCRILWDSDILCLPGDIVPAPGPVLAPTHLQTELVL  
LRCQKETDCDLCLRVAVHLAVGHWEEPEDEEKFGGAADSGVVEPRNASLQAQVVLFSQAYPTARCVILLEV  
QVPAALVQFGQSVGSVYYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSADGDNVHLVILNVS  
EEQHFGLSLYWNQVQGPPKPRWHKNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQN  
LWQAARLRLLTLQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKLEFPLLKGHPNLCVQ  
VNSSEKLQLQECIWLADSLGPLKDDVLLLETRGPQDNRSILCALEPSGCTSLPSKASTRAARLGEYLLQDLQS  
GQCLQLWDDDLGALWACPMKYIHKRWALVWLACLLFAAALSLLLLKKDHAKGWLRLKQDVRSGAAARG  
RAALLLYSADDSGFERLVGALASALCQLPLRVAVLWSRRELSAQGPVAFHQAQRRQTLQEGGVVVLLFSP  
GAVALCSEWLQDGVSQPGAHGPDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTPVVF  
LPSQLPDFL GALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPAGPGAGDGT

**Signal sequence:**

amino acids 1-20

**Transmembrane domain.**

amino acids 453-475

**N-glycosylation sites.**

amino acids 118-121, 186-189, 198-201, 211-214, 238-241, 248-251,  
334-337, 357-360, 391-394

**Glycosaminoglycan attachment site.**

amino acids 583-586

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 552-555

**N-myristoylation sites.**

amino acids 107-112, 152-157, 319-324, 438-443, 516-521, 612-617,  
692-697, 696-701, 700-705

## FIGURE 163

GGGAGGGCTCTGTGCCAGCCCCATGAGGACGCTGTGACCATTTGACTGTGGGATCCCTGGCT  
GCTCACGCCCTGAGGACCCCTCGGATCTGCTCCAGCACGTGAAATTCCAGTCCAGCACTTGA  
AAACATCCTGACGTGGACAGGGGGCAGAGGGCACCCAGACACGGTCTACAGCATCGAGTATA  
AGACGTACGGAGAGAGGGACTGGGTGGCAAAGAAGGGCTGTCAGGGATCACCCGGAAAGTCC  
AACCTGACGGTGGAGACGGGCAACCTCACGGAGCTCTACTATGCCAGGGTACCGCT  
GTCAGTGCAGGGGGGGTCAGCCACCAAGATGACTGACAGGTTCAAGCTCTGCAGCACACTAC  
CCTCAAGCCACCTGATGTGACCTGTATCTCAAAGTGGAGATCGATTCAAGATGATTGTCATC  
CCCCCACGCCAACCGCACTGGGCTAACCGTGGAAAGACATCTTCCATGACCTG  
TTCTACCACTAGAGCTCCAGGTCAACCGCACCTACCAAATGCACCTTGGAGGGAAAGCAGAGA  
ATATGAGTTCTCGGCCTGACCCCTGACACAGAGTCCCTGGCACCATCATGATTGCGTT  
CCTGGGCAAGGAGAGTGGCCCTACATGTGCCAGTGAAGACACTGCCAGCCGACATGGACC  
TACTCCTCTCCGGAGCCTTCTGTATCTCCATGGGCTCTCGTCAGTACTCTGCTACCTGAG  
CTACAGATATGTACCAAGCCGCTGCACCTCCAACTCCCTGAACGTCAGCGAGTCTGACTT  
TCCAGCCGCTGCGCTTATCCAGGAGCACGTCTGATCCCTGTCTTGACCTCAGCGGGCCCCAGC  
AGTCTGGCCAGCCTGTCAGTACTCCCAGATCAGGGTCTGGACCCAGGGAGCCCGCAGGAGC  
TCCACAGCGGATAGCCTGTCAGGATCACCTACTTAGGGCAGCCAGACATCTCATCCTCCAGC  
CCTCCAACGTGCCACCTCCCCAGATCCTCTCCCACTGCTCATGGCCCAAACGCTGCCCTGAG  
GTCGGGGCCCCATCCTATGCACCTCAGGTGACCCCCGAAGCTCAATTCCATTCTACGCC  
GGCCATCTAAGGTCCAGCCTCCCTATGCCCTCAAGCACTCCGGACAGCTGGCCTCC  
CCTATGGGTATGCATGGAAAGGTTCTGGCAAAGACTCCCCACTGGGACACTTCTAGTCTAA  
CACCTTAGGCCTAAAGGTAGCTTCAGAAAGAGCCACAGCTGGAGCTGATGTTAGGTGCC  
TTCTCTGCAAGGAGGTGACCTCTGGCTATGGAGGAATCCAAAGAAGCAAATATTGCA  
CCCTGGGATTGCAAGACAGAACATCTCACCCAAATGTGCTACACAGTGGGAGGAAGGGACA  
CCACAGTACCTAAAGGGCCAGCTCCCCCTCCTCTCAGTCAGATCGAGGGGCCACCCATGTC  
CCTCCCTTGCAACCTCTTCCGGTCCATGTTCCCTCGGACCAAGGTCCAAGTCCCTGGG  
TGCTGGAGTCCCTGTGTGTCAGGATGAAGCCAAGGCCAGGGCTGAGACCTCAGACCTG  
GAGCAGCCCACAGAAGTGGATTCTCTGGCTAGAGGCTGGCCCTGACTGTGCA  
AGGGGAATGGGAAAGGCTGGCTCTCTCTGCTCCCTACCCAGTGTCA  
ATCCCAGCTGCCATGCCACACACTCTGCGATCTGGCCTCAGACGGGTGCC  
AGAGGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCTCACCG  
AGAGGAGTGGCATGCAGGGCCCTGCCATGGGTGCGCTCTCACCG  
CAAGGAGAAATGACAGTGCAGGAGGAATGCAGGGAAACTCC  
GAGGTCCAAGGCCAGGGCTGAGCTGAGACAGCAGT  
CTAACACCATGGATTCAAAGTGCAGGGAAATTG  
CTGCTCTGCCCTGCTCTGTCA  
ACAATCTAGCTGCAGAGCATGAGGCCCTGCC  
ACTGGAAAAGAACCGGCCAGGGAAAGAAC  
CAGAGGAGGCTGGCAGAAC  
GCCTGGAAAAGAACCGGCCAGGGAAAGAAC  
CAGAGGAGGCTGGCAGAAC  
ACTTCTGCCAAGGCCAGGGCCAGCAGGAGGGACTCTAGGGAGGGTGT  
GGCCTGCAGCTCA  
TTCCCAAGGCCAGGGCAACTGCC  
CTGCTGACGTTGACGATT  
CAGCTTCAGCTTCTG  
GATAGAACAAAGC  
GAAATGCAGGTCC  
CTAACAGCTGTG  
ACTTCAAA  
ACAATGAA  
AGGAGTGG  
GAGGGCTG  
GGCCCTGG  
ACGGGT  
ACAATAAC  
AC  
TGTACTG  
ATGT  
CACA  
AGCT  
GTG  
ACTT  
CAAA  
ACA  
AA  
ATG  
TAA  
AGT  
GCT  
TA  
AGT  
GC  
CT  
GG  
GT  
AC  
ATG  
GGG  
CAG  
GCC  
AA  
AA  
ACGGT  
AGCT  
ATTT  
AAAA  
AAAAAAA

## **FIGURE 164**

MRTLLTILTVGSLAAHAPEDPSDLLQHVKFQSSNFENILTWDSGPEGTPDTVYSIEYKTYGERDW  
VAKKGCQRITRKSCNLTVETGNLTLYYARVTAVSAGGRSATKMTDRFSSLQHTTLKPPDVT CIS  
KVRSIQMIVHPTPTPIRAGDGHRLTLEDIFHDLFYHLELQVNRTYQMHLGGKQREYEFFGLTPDT  
EFLGTIMICVPTWAKESAPYMCRVKTLPDRTWTYSFSGAFLFSMGFLVAVLCYLSYRYVTKPPAP  
PNSLNQVRVLTQPLRFIQEHVLIPVFDLSPGSSLAQPVQYSQIRVSGPREPAGAPQRHSLSEIT  
YLGQPDISILQPSNVPPPQILSPLSYAPNAAPEVGPPSYAPQVTPEAQFPFYAPQAIISKVQPSY  
APQATPDSWPPSYGVCMEGSGKDSPTGTLSSPKHLRPKGQLOKEPPAGSCMLGGSLQEVTS LAM  
EESQEAKSLHQPLGICTDRTSDPNVLHSGEEGTPQYLGQLPLLSSVQIEGHPMSLPLQPPSGPC  
SPSDQGPSPWGLLESLVCPKDEAKSPAPETSDLEQPTELDSLFRGLALT VQWES

**Signal sequence.**

amino acids 1-17

**Transmembrane domain.**

amino acids 233-250

**N-glycosylation sites.**

amino acids 80-83, 87-90, 172-175

**N-myristoylation sites.**

amino acids 11-16, 47-52, 102-107, 531-536, 565-570

## **FIGURE 165**

TGGCCTACTGGAAAAAAAAAAAAAGTCACCCGGGCCCGCGTGGCCACAACATGG  
CTGCGGCGCCGGGCTGCTCTCTGGCTGTCGTGGGGCGCTCTGGTGGGTCCCAG  
TCGGATCTCAGCCACGGACGGCGTTCTGGACCTCAAAGTGTGCGGGGACGAAGAGTGCAGCAT  
GTTAATGTACCGTGGGAAAGCTTGAAGACTTCACGGCCCTGATTGTCGTTGTGAATT  
AAAAAGGTGACGATGTATATGTTACTACAAACTGGCAGGGGATCCCTGAAC  
TTGGCTGGA  
AGTGTGAACACAGTTGGATATTTCCAAAAGATTGATCAAGGTACTTCATAAATACACGGA  
AGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCGCTTGAGGAGGAAGAGATGATT  
TTAATAGTTATAATGAGAGCTTTAGGATCTTGGA  
ACTGGAGGACTCTGTACCTGAAGAG  
TCGAAGAAAGCTGAAGAAGTTCTCAGCACAGAGAGAAATCTCCTGAGGAGTCTCGGGGGCGTGA  
ACTTGACCCCTGTGCCTGAGCCCGAGGCATTCA  
GAGCTGATTCA  
GAGGATGGAGAAGGTGCTTCT  
CAGAGAGCACCGAGGGGCTGCAGGGACAGCCTCAGCTCAGGAGAGCCACCC  
CACACCAGCGGT  
CCTGC  
GGCTAACGCTCAGGGAGTGCAGTCTCGTGGACACTTTGAAGAAATTCTGCACGATAA  
ATTGAAAGTGC  
CGGGAAAGCGAAAGCAGAAC  
TGGCA  
ATAGTTCTCGCTCGTGGAGCAGTGGACAGTGC  
GTTATT  
AGACAGATGCTTACAAAGTC  
CTGAAAACAGAAATGAGTCAGAGAGGAAGTGGACAGTGC  
GTTATT  
CATTACAGCAAAGGATT  
TCGTTGCAT  
CAAATCTAAGTTGTTACAAAGATTGTTT  
TAGTA  
CTAAGCTGCCTGGCAGTTGCATT  
TTGAGCCA  
ACAAAAATATATT  
ATT  
TTCCCTCTAAGTA  
AAAAAA

## **FIGURE 166**

MAAAPGLLFWLFWLGALWWVPGQSDLSHGRRFSDLKVCGLDEECMILMYRGKALEDFTPDCRFVN  
FKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEELHIPADEDFVCFEGGRD  
DFNSYNVEELLGSLEEDSVPEESKKAEEVSQHREKSPPEESRGRELDPVPEPEAFRADSEDEGA  
FSESTEGLQGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDKLKVPGSESRTGNSSPASVER  
EKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYKDCF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**N-glycosylation site.**

amino acids 294-298

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34

**Tyrosine kinase phosphorylation site.**

amino acids 67-76

**N-myristoylation sites.**

amino acids 205-211, 225-231, 277-283

**Amidation site.**

amino acids 28-32

## **FIGURE 167**

CCAGGACCAGGGCGCACCGGCTCAGCCTCTACTGTCAGAGGCCGGGAAGAGAACGAAAGCGC  
AACGGTGTGGTCCAAGCCGGGCTCTGCTCGCCTCTAGGACATACACGGGACCCCTAACCTTC  
AGTCCCCAAACGCCACCCCTCGAAGTCTTGAACCTCCAGGCCGCACATCCACGCCGGCACAGG  
CGCGCAGGCCGGCAGGTCCCAGGCCGAAGGCCATGCCGCCAGGGGGTCGGGCCAGCTGGCTCGGGC  
GGCAGGGAGTAGGGCCCGGCAGGGAGGCCAGGGAGGCTGCATATTCAAGAGTCGGGGCTGCCCTG  
GGCAGAGGCCGCCCTCGCTCCACGCAACACTGCTGCTGCCACCGGCCGGCAGTGGCCGTGG  
TCTCGCTGCTGCTGGCGCCGCGCTGCTCGGCCACGGAGCCTCTGCCGCCGTGGTCAGC  
GCCAAAAGGTGTGTTTGCTGACTTCAAGCATCCCTGCTACAAAATGGCCTACTTCCATGA  
GTCCAGGCCAGTGAAGCTTCAAGGACGCCCTGGCTTGAGAGTGAGGGAGGAGTCCTCTCA  
GCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAGAGCATGTTGCAAAACCTGACAAAACCCGGG  
ACAGGGATTCTGTGGTATTCTGGATAGGGCTTGGAGGAATGGAGATGGGAAACATCTGG  
TGCCTGCCAGATCTTACCAAGTGGTCTGATGGAAGCAATTCCAGTACCGAAACTGGTACACAG  
ATGAACCTCCCTGCGGAAGTGAAGGAAAGTGTGTTGTATGACCAACCAACTGCCAACCTGGC  
CTTGGGGTCCCTACCTTACCAAGTGGAAATGATGACAGGGTGAACATGAAGCACAATTATTTG  
CAAGTATGAACCAGAGATTAATCCAACAGCCCTGAGAAAAGCCTATCTTACAATCAACAG  
GAGACACCCATCAGAATGTGGTGTACTGAAGCAGGTATAATTCCAATCTAATTATGTTGTT  
ATACCAACAATACCCCTGCTTACTGATACTGGTTGCTTTGGAACCTGTTGTTCCAGATGCT  
GCATAAAAGTAAGGAAGAACAAAAGTACGCTAACACCAGTCTACACTGTGGATTCAAAGAGTA  
CCAGAAAAGAAAGTGGCATGGAAGTATAAACTCATGGACTTGGTCCAGAATTGGTAAATTCT  
GGATCTGTATAAGGAATGGCATCAGAACAAATAGCTTGGAAATGGCTGAAATCAAAGGATCTG  
AAGATGAACGTAAAGCTCCCCCTGAGGCAAAATTAAAGTAATTTTATATGCTTAAAGGATGCT  
TTTAAAGAATATGCTGTGCTAAATGGAGTGAGACATGCTTATTGCTAAAGGATGCCCAA  
ACTTCAAACCTCAAGCAAATGAAATGGACATGCAGATAAAAGTGTATCAACACGTCGGGAGTA  
TGTGTGTTAGAAGCAAATCCTTTATTCTTCACCTTCATAAGTGTATCTAGTCAATGTA  
TGTATATTGTATTGAAATTACAGTGTGCAAAAGTATTTCACCTTGCATAAGTGTGTTGATA  
ATGAACCTGTTCAATATTATTATTGACATCTCATTTCAATACATGCTTTGATTAAAG  
AAACTTAACTACTGTGTCAACTGAATTCACACACACACAAATATAAGTACCATAGAAAAGTTGT  
TTCTCGAAATAATTCACTTTCAGCTCTGCTTTGGTCAATGCTAGGAAATCTTCAGA  
AATAAGAAGCTATTCAATTAAAGTGTGATATAACCTCCCAAACATTTACTTAGGAGGAT  
TGTCTAATTCAATTGTGCAAGACATGTGCTTATAATTATTTAGCTTAAACAGATT  
TTGTAATTCAATTGTAATTGCTTAAAGGTGCTAAACACTAATGCAATTGAAACAAAAGAAG  
TGACATACACAAATAAAATCATATGCTTACACAGTGGCTTATAATGAGAACGAGCTCTGA  
GGGTTCTGAAATCAATGTGGCTCTCTTGCCTAAACACAAAGATGGTTGTTGGGGTTGG  
ATTGACACTGGAGGCAGATAGTGCAGAAAGTTAGTCTAAGGTTCCCTAGCTGTTAGCTCTG  
ACTATATTAGTATACAAGAGGTCACTGTGGTGGAGACAGGTAATAGTCACTATCAGTGTGGAG  
ACAAGCACAGCACACAGACATTAGGAAGGAAGGAACATCGAAATCGTGTGAAATGGGTTGG  
AACCCATCAGTGATCGCATATTCAATTGATGAGGGTTGCTGAGATAGAAAATGGTGGCTCTT  
CTGTTCTATCTCTAGTTCTCAATGCTTACGCCCTGTTCTCTCAAGAGAAAGTTGTAAC  
CTGGTCTTCAATATGCTTGTGCTCCCTTAAACAAATAAAAGAGTTCTGTTCTGGGGAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 168**

MSRVVSLLLGAALLCGHGAFCRVVSGQKVCADFHKPCYK MAYFHELSSRVSFQEARLACESE  
GGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDGSNSQ  
YRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINPTAPVEK  
PYLTNQPGDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKGRTKTSPNQ  
STLWISKSTRKESGMEV

**Important features of the protein:**

**Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 214-235

**N-glycosylation sites.**

amino acids 86-89, 255-258

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

**N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145, 212-217